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OM protein - protein search, using sw model

Run on: January 29, 2004, 14:06:57 ; Search time 46 Seconds
(without alignments)
1507.902 Million cell updates/sec

Title: US-09-941-947a-2
Perfect score: 2284
Sequence: 1 DVTWTPYHLRADIRFCWHPF.....FNSMLSEIGQPKGKVEVSH 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2004.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	2284	100.0	437	23 ABG61553
2	2284	100.0	437	23 ABG61553
3	2284	100.0	437	23 ABG61553
4	2284	100.0	437	23 ABG61553
5	2284	100.0	437	23 ABG61553
6	2284	100.0	437	23 ABG61553
7	2284	100.0	437	23 ABG61553
8	2284	100.0	437	23 ABG61553
9	2284	100.0	437	23 ABG61553

10	262	11.5	485	16 AAR71579
11	257.5	11.3	500	23 ABB93109
12	251	11.0	473	21 AAG36438
13	251	11.0	473	21 ABB93145
14	251	11.0	537	21 AAG36437
15	247	10.6	366	21 AAG39481
16	243	10.6	462	23 ABB93203
17	240.5	10.5	320	22 AAU38192
18	239	10.5	462	21 AAG28969
19	239	10.5	489	21 AAG28968
20	238.5	10.4	320	22 AAU34629
21	234	10.2	509	21 AAG47222
22	234	10.2	525	23 ABB93912
23	232	10.2	462	22 AAU42927
24	226.5	9.9	320	22 AAU36128
25	226.5	9.9	345	23 ABB38929
26	226.5	9.9	444	23 ABB93134
27	222.5	9.7	322	22 AAU33929
28	222.5	9.7	322	22 AAU37026
29	222.5	9.7	322	22 AAU37314
30	222	9.7	340	23 ABB54672
31	221	9.7	335	21 AAU37753
32	220.5	9.7	353	21 AAG36439
33	219.5	9.6	375	22 AAG35420
34	218.5	9.6	320	22 AAU35056
35	216	9.5	337	23 ABB27458
36	215	9.4	335	24 ABB81576
37	215	9.4	335	24 ABB01294
38	211.5	9.3	522	16 AAR71582
39	211	9.2	340	23 ABB27457
40	210.5	9.2	544	21 AAU57302
41	210	9.2	780	24 ABB07399
42	206.5	9.0	781	18 AAU11298
43	205	9.0	342	21 AAG28970
44	204.5	9.0	795	22 ABB06051
45	204	8.9	463	23 ABB91839

ALIGNMENTS

RESULT 1	ABG61553	High growth methanotrophic bacterial strain: Ci carbon substrate; enzyme: methane; methanol; Embden-Meyerhof carbon flux pathway; 16S rRNA; pyrophosphate dependent phosphotrioxinase; nitrogen-containing compound; ammonia; nitrate; nitrite; nitrogen; pigment; oxygen; landfill; methane-containing environment; waste water treatment system; isoprenoid; nitrous oxide; terpenoid; animal feed; carotenoid; exopolysaccharide.
OS	Methylobionas sp.	
XX	WO200220728-A2.	
XX	14-MAR-2002.	
XX	28-AUG-2001; 2001WO-US26827.	
XX	01-SRP-2000; 2000US-229858P.	
XX	(DUPO) DU PONT DE NEMOURS & CO E I.	
XX	Kofas M, Odum JM, Schenzle A;	
XX	WPI; 2002-452200/48.	

DR N-PSDB; ABK83232.

XX New high growth methanotrophic bacterial strain, useful for producing
 FT single cell proteins, grows on a C1 carbon substrate, and comprises a
 PT functional gene encoding in Embden-Meyerhof carbon pathway

PS Claim 7; Page 85-87; 157pp; English.

XX The invention relates to a high growth methanotrophic bacterial strain,
 CC which grows on a C1 carbon substrate e.g. methane and methanol, and
 CC comprises a functional Embden-Meyerhof carbon flux pathway comprising a
 CC gene coding a pyrophosphate dependent phosphotransferase enzyme or a 16s
 CC rRNA. The bacterial strain is useful for the production of single cell
 CC protein and for the biotransformation of a nitrogen-containing compound,
 CC e.g. ammonia, nitrate, nitrite or nitrogen. It is also useful for the
 CC production of a feed product comprising a protein, carbohydrates and a
 CC pigment and for reducing oxygen demand, for removing nitrates and
 CC nitrates in methane-containing environments such as landfills, waste
 CC water treatment systems or anywhere that methane, oxygen and nitrates are
 CC present. The bacterial strain of the invention can be used as a
 CC denitrifying agent for the conversion of nitrate or nitrite to nitrous
 CC oxide with methane or methanol as a carbon source. It is also used in the
 CC production of biomass including proteins, carbohydrates and a wide
 CC variety of pigments (particularly for isoprenoid pigments for the
 CC purpose of generating animal feeds), in production of terpenoid and
 CC carotenoid compounds, useful as pigments and as monomers in polymeric
 CC materials and in production of exopolysaccharides at high levels.
 CC Sequences ABG61551-ABG61590 represent high growth methanotrophic
 CC bacterial strain proteins of the invention.

XX Sequence 437 AA;

Query Match 100.0%; Score 2284; DB 23; Length 437;

Best Local Similarity 100.0%; Pred. No. 2e-207;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVTWPHYLLADIRFCGMPFNFTLNKPKKVAIITAGGLAPCLNSAIGLIERYTE 60
 DB 1 DVTWPHYLLADIRFCGMPFNFTLNKPKKVAIITAGGLAPCLNSAIGLIERYTE 60
 QY 61 IDPSIEIICYRGYKGLLGDSPVTAVERKKAQVLRFGGSVIGNSRVKLTNVKDCVCR 120
 DB 61 IDPSIEIICYRGYKGLLGDSPVTAVERKKAQVLRFGGSVIGNSRVKLTNVKDCVCR 120
 QY 121 GLVKEGDDPOKVAADQVLDGVDILFTIGDDDTNTAAADLAAPLARNNGGLTVIGPKTV 180
 DB 121 GLVKEGDDPOKVAADQVLDGVDILFTIGDDDTNTAAADLAAPLARNNGGLTVIGPKTV 180
 QY 121 GLVKEGDDPOKVAADQVLDGVDILFTIGDDDTNTAAADLAAPLARNNGGLTVIGPKTV 180
 DB 121 GLVKEGDDPOKVAADQVLDGVDILFTIGDDDTNTAAADLAAPLARNNGGLTVIGPKTV 180
 QY 181 DNDVFPKISLGAMTAAGQARYFNANVVAENNANPRMLIVHEVWGNCGMLTAATQOBYR 240
 DB 181 DNDVFPKISLGAMTAAGQARYFNANVVAENNANPRMLIVHEVWGNCGMLTAATQOBYR 240
 QY 241 KLIDRAEWPELGLTRSEYEVHANVFPMAIDLAENKRLAEVNDKDCVNIPISEBAGY 300
 DB 241 KLIDRAEWPELGLTRSEYEVHANVFPMAIDLAENKRLAEVNDKDCVNIPISEBAGY 300
 QY 301 EAIIVEMAKOQOEVRDPAFGIKLDAVNGKMFQGFQOMIGAKETLVOKSGYFARASAS 360
 DB 301 EAIIVEMAKOQOEVRDPAFGIKLDAVNGKMFQGFQOMIGAKETLVOKSGYFARASAS 360
 QY 361 NVDDMRLLIKSCADLAVECAFRESGVIGHDEEDNGVLAIEFPRIKGGKFNITDWPNS 420
 DB 361 NVDDMRLLIKSCADLAVECAFRESGVIGHDEEDNGVLAIEFPRIKGGKFNITDWPNS 420
 QY 421 MLSEIIGQPKGKQVEVSH 437
 DB 421 MLSEIIGQPKGKQVEVSH 437

RESULT 2
 ID AAE22299
 XX AAE22299 standard; Protein; 437 AA.

AC AAE22299;

XX 25-JUL-2002 (first entry)

DE Methylomonas 16a sp. phosphofructokinase pyrophosphate dependent enzyme.

XX Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astataxanthin; diet;
 KM anti-oxidant; steroid; fragrance; electro-optic application;
 KM aquaculture; enzyme; phosphofructokinase pyrophosphate.

XX Methylomonas 16a sp.

XX WC200218617-A2.

XX 07-MAR-2002.

XX 04-SEP-2001; 2001MO-US27420.

XX 01-SEP-2000; 2000US-229858P.

XX 01-SEP-2000; 2000US-229907P.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

XX Brzostowicz PC, Cheng Q, Dicosimo DJ, Koffas M, Miller ES;

XX Odum JM, Picataccio SK, Rouviere PB;

XX WPI; 2002-351711/38.

XX N-PSDB; AAD35497.

XX Producing carotenoid compounds e.g. antheraxanthin and astataxanthin, by
 PT using microorganisms having a nucleic acid molecule encoding enzymes in
 PT the carotenoid biosynthetic pathway and which metabolize single carbon
 PT substrates

PS Claim 8; Page 104-106; 156pp; English.

XX The invention relates to a method for producing carotenoid compounds.
 CC The method comprises a transformed metabolizing host cell, comprising
 CC suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule
 CC encoding an enzyme in the carotenoid biosynthetic pathway, under the
 CC control of regulatory sequences, and contacting the host cell with carbon
 CC substrate to produce a carotenoid compound. The method is useful for
 CC producing carotenoid compounds such as antheraxanthin and astataxanthin, by
 CC using microorganisms having a nucleic acid molecule encoding enzymes in
 CC the carotenoid biosynthetic pathway and which metabolize single carbon
 CC substrates. The carotenoids have potent anti-oxidant properties useful in
 CC diet, and aquaculture elements. The carotenoids are also useful as
 CC intermediates in the synthesis of steroids flavours and fragrances and
 CC compounds for potential electro-optic applications. The present sequence
 CC is Methylomonas 16a sp. phosphofructokinase pyrophosphate dependent
 CC enzyme used in the invention.

XX Sequence 437 AA;

Query Match 100.0%; Score 2284; DB 23; Length 437;

Best Local Similarity 100.0%; Pred. No. 2e-207;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVTWPHYLLADIRFCGMPFNFTLNKPKKVAIITAGGLAPCLNSAIGLIERYTE 60
 DB 1 DVTWPHYLLADIRFCGMPFNFTLNKPKKVAIITAGGLAPCLNSAIGLIERYTE 60
 QY 61 IDPSIEIICYRGYKGLLGDSPVTAVERKKAQVLRFGGSVIGNSRVKLTNVKDCVCR 120
 DB 61 IDPSIEIICYRGYKGLLGDSPVTAVERKKAQVLRFGGSVIGNSRVKLTNVKDCVCR 120
 QY 121 GLVKEGDDPOKVAADQVLDGVDILFTIGDDDTNTAAADLAAPLARNNGGLTVIGPKTV 180
 DB 121 GLVKEGDDPOKVAADQVLDGVDILFTIGDDDTNTAAADLAAPLARNNGGLTVIGPKTV 180
 QY 181 DNDVFPKISLGAMTAAGQARYFNANVVAENNANPRMLIVHEVWGNCGMLTAATQOBYR 240
 DB 181 DNDVFPKISLGAMTAAGQARYFNANVVAENNANPRMLIVHEVWGNCGMLTAATQOBYR 240

QY 241 KLDRAEWLPELGLTRBSYEYHAFVPEMAIDLEAKRLREVMKVCVNI FVSEBAGV 300
 DB 241 KLDRAEWLPELGLTRBSYEYHAFVPEMAIDLEAKRLREVMKVCVNI FVSEBAGV 300
 QY 301 EAIYAEWAKQGEVPRDPAFGHITKLDVNPGRKFGSGPQAMIGAKETLVXKSGYFARASAS 360
 DB 301 EAIYAEWAKQGEVPRDPAFGHITKLDVNPGRKFGSGPQAMIGAKETLVXKSGYFARASAS 360
 QY 361 NVDDMRLLKSCADLAVECAFRBSGVIGHDEDNQVLAIEFPRIKGGKPFNIDTWFNS 420
 DB 361 NVDDMRLLKSCADLAVECAFRBSGVIGHDEDNQVLAIEFPRIKGGKPFNIDTWFNS 420
 QY 421 MLSEIGQPKGKVEVSH 437
 DB 421 MLSEIGQPKGKVEVSH 437
 RESULT 3
 ABB09168 standard; Protein; 437 AA.
 ID ABB09168;
 AC ABB09168;
 XX 01-JUL-2002 (first entry)
 DT 01-JUL-2002 (first entry)
 DE Methylomonas pyrophosphate dependent phosphofructokinase SEQ ID NO.16.
 XX Methylomonas; methanotropic; carbon metabolism; carbon flux pathway;
 KM transaldolase; fructose biphosphate aldolase; KMG/KDPG aldolase; food;
 KM pyrophosphate dependent phosphofructokinase; phosphoglucumutase; feed;
 KM glucose 6 phosphate isomerase; 6-phosphogluconate dehydratase; methane;
 KM glucose 6 phosphate 1 dehydrogenase; enzyme; methanotroph; methanol;
 KM single carbon substrate; single cell protein; polysaccharide; thickener;
 KM isoprenoid; carotenoid pigment.
 XX
 OS Methylomonas sp.
 XX WO200220796-A2.
 XX 14-MAR-2002.
 PD 28-AUG-2001; 2001WO-US26730.
 PF 01-SEP-2000; 2000US-229906P.
 PR (DUPO) DU POINT DE MEMOIRS & CO E I.
 PA Koffas M, Odum JM, Norton KC, Ye RW;
 PI MPI: 2002-362250/39.
 DR N-PSDB; ABUS1513.
 XX
 PT New polynucleotide encoding a Methylomonas sp. carbon flux enzyme
 PT useful for altering carbon flow through methanotrophic bacteria,
 PT utilized for production of single cell protein and commercially
 PT valuable polysaccharides -
 XX
 PS Claim 4; Page 66-68; 73pp; English.
 CC The present invention describes isolated polynucleotides (I) encoding a
 CC Methylomonas sp. carbon flux enzyme, consisting of: transaldolase;
 CC fructose biphosphate aldolase; KMG/KDPG aldolase; phosphoglucumutase;
 CC pyrophosphate dependent phosphofructokinase; glucose 6 phosphate
 CC isomerase; 6-phosphogluconate dehydratase; and glucose 6 phosphate 1
 CC dehydrogenase enzymes. (i) overexpression is useful for altering carbon
 CC flow through a methanotrophic bacteria, where the bacteria grows on a C1
 CC carbon substrate of methane and methanol, and comprises a functional
 CC Embden-Meyerhof carbon pathway comprising a gene encoding a pyrophosphate
 CC dependent phosphofructokinase enzyme, where the bacteria is preferably
 CC Methylomonas 16a American Type Culture Collection (ATCC) PTA 2402, and
 CC where the carbon flux gene is: (i) over-expressed on a multicopy plasmid;
 CC (ii) operably linked to an inducible or regulated promoter;

CC (iii) expressed in an antisense orientation; or (iv) disrupted by
 CC insertion of foreign DNA into the coding region. The manipulated
 CC methanotrophs are useful for the energy efficient conversion of single
 CC carbon substrates such as methane and methanol to commercially useful
 CC products in the food, feed and materials industries, and preferably for
 CC the production of single cell protein, and for producing polysaccharides,
 CC used as thickeners in food and non-food industries, and isoprenoid
 CC compounds and carotenoid pigments of various carbon lengths. The present
 CC sequence represents a Methylomonas pyrophosphate dependent
 CC phosphofructokinase from the present invention.
 XX
 SQ Sequence 437 AA;
 Query Match 100.0%; Score 2284; DB 23; Length 437;
 Best Local Similarity 100.0%; Pred. No. 2e-207;
 Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVYMPYHLTADIFGCHWFILNFPYTLANKPKYAILTAGGLAPCLNSAIGSLIERYTE 60
 DB 1 DVYMPYHLTADIFGCHWFILNFPYTLANKPKYAILTAGGLAPCLNSAIGSLIERYTE 60
 QY 61 IDPSIELICRYGKYKGLLDGSDYPVLAVERKAGVLRFGSGVIGNSRVKLTNVDCYKR 120
 DB 61 IDPSIELICRYGKYKGLLDGSDYPVLAVERKAGVLRFGSGVIGNSRVKLTNVDCYKR 120
 QY 121 GLVKEGEDPQRYAADQLVKQGVDTLHTIGGDDTNTAADLAFLARNYGLTVIGLPTV 180
 DB 121 GLVKEGEDPQRYAADQLVKQGVDTLHTIGGDDTNTAADLAFLARNYGLTVIGLPTV 180
 QY 181 DNDVFPRIQSGIANTAAEGARFYNNVAENNAAPRLIIVHEVGRNCGMTAAATQERYR 240
 DB 181 DNDVFPRIQSGIANTAAEGARFYNNVAENNAAPRLIIVHEVGRNCGMTAAATQERYR 240
 QY 241 KLDRAEWLPELGLTRBSYEYHAFVPEMAIDLEAKRLREVMKVCVNI FVSEBAGV 300
 DB 241 KLDRAEWLPELGLTRBSYEYHAFVPEMAIDLEAKRLREVMKVCVNI FVSEBAGV 300
 QY 301 EAIYAEWAKQGEVPRDPAFGHITKLDVNPGRKFGSGPQAMIGAKETLVXKSGYFARASAS 360
 DB 301 EAIYAEWAKQGEVPRDPAFGHITKLDVNPGRKFGSGPQAMIGAKETLVXKSGYFARASAS 360
 QY 361 NVDDMRLLKSCADLAVECAFRBSGVIGHDEDNQVLAIEFPRIKGGKPFNIDTWFNS 420
 DB 361 NVDDMRLLKSCADLAVECAFRBSGVIGHDEDNQVLAIEFPRIKGGKPFNIDTWFNS 420
 QY 421 MLSEIGQPKGKVEVSH 437
 DB 421 MLSEIGQPKGKVEVSH 437
 RESULT 4
 AAU45865 standard; Protein; 410 AA.
 ID AAU45865;
 AC AAU45865;
 XX 27-FEB-2002 (first entry)
 DT 27-FEB-2002 (first entry)
 DE Propionibacterium acnes immunogenic protein #6761.
 XX
 XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 XX uveitis; endophthalmitis; bone; joint; central nervous system; EUSA;
 KM inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KM dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX WO200181581-A2.
 XX 01-NOV-2001.
 XX 20-APR-2001; 2001WO-US12865.

21-APR-2000; 2000US-199047P.
 ER 02-JUN-2000; 2000US-208841P.
 ER 07-JUL-2000; 2000US-216747P.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Skeiky YAM, Pearing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'waisomeuve J, Zhang Y, Jen S, Carter D;
 DR MPI; 2001-616774/71.
 XX N-PSDB; AAS59528.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 PS Example 1; SEQ ID NO 7060; 1069pp; English.
 XX
 CC Sequences AAU9105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SO Sequence 410 AA;
 Query Match 63.1%; Score 1442; DB 22; Length 410;
 Best Local Similarity 68.6%; Pred. No. 1e-127;
 Matches 271; Conservative 54; Mismatches 70; Indels 0; Gaps 0;
 QY 33 KKVALLTAGGLAPCNSAIGSLIERYTEIDPSIEIICRGQYKGLGDSYPYATVRKK 92
 DB 15 KKVALLTAGGLAPCNSAIGSLIERYTEIDPSIEIICRGQYKGLGDSYPYATVRKK 74
 QY 93 AGVLQRFQGSVIGNSRVKLTNVKDCVVRGLVKEGEDPQKVAADQLVXGVDILHTIGSD 152
 DB 75 AEIILKRFQGSPIGNSRVKLTNVKDCVVRGLVKEGEDPQKVAADQLVXGVDILHTIGSD 134
 QY 153 TTTTAAADLAALFANNNGLTIVIGLPTVNDVPPFIKOSLGAWTAAGQARYFMVVAEN 212
 DB 135 TTTTAAADLAALFANNNGLTIVIGLPTVNDVPPFIKOSLGAWTAAGQARYFMVVAEN 194
 QY 213 ANPEMLIVHEVWGNCGWLTAAOBYRKLDRAEMLPELGLTRSEYVAHVPPEVAID 272
 DB 195 SGGSWLIVHEVWGNCGWLTAAOBYRKLDRAEMLPELGLTRSEYVAHVPPEVAID 254
 QY 273 LEAAKRLREVMKDCVNTIVSFGAGYEAIVAEKQAGQEVPPDAAGHKLDAVNGK 332
 DB 255 LEAAKRLREVMKDCVNTIVSFGAGYEAIVAEKQAGQEVPPDAAGHKLDAVNGK 314
 QY 333 FGEFOAQMIGAEKTLVQKSGYFARASASNVDMILIKSCADLAECAPRESGYLGHD 392
 DB 315 FGEFOAQMIGAEKTLVQKSGYFARASASNVDMILIKSCADLAECAPRESGYLGHD 374
 QY 393 NGNVLRAIEPRIRKGRPFNIOTDWNSTSEIQ 427
 DB 375 NGNVLRAIEPRIRKGRPFNIOTDWNSTSEIQ 409

RESULT 5
 ABB93840
 ID ABB93840 standard; Protein; 488 AA.
 XX
 XX ABB93840;
 AC
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE Herbicidally active polypeptide SEQ ID NO 3051.
 XX
 KM Herbicidal; plant; agriculture; herbicide.
 XX
 OS Arabidopsis thaliana.
 XX
 PN W0200210210-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 28-AUG-2001; 2001WO-EP09892.
 XX
 PR 28-AUG-2001; 2001WO-EP09892.
 XX
 PA (PARB) BAYER AG.
 XX
 PI Tietjen K, Weidler M;
 DR MPI; 2002-269010/31.
 XX
 PT Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 PT organisms -
 XX
 PS Claim 5; SEQ ID NO 3051; 261pp + Sequence listing; English.
 XX
 CC The invention relates to identifying target proteins
 CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
 CC aligning and comparing nucleic acid or amino acid sequences from plant
 CC with nucleic acid or amino acid sequences from non-plant organisms using
 CC suitable search parameters, where plant sequences having an E-value
 CC greater by a factor of 3 than the B-value of most similar non-plant
 CC sequences are selected. The polypeptides or nucleic acids encoding them
 CC are useful for identifying modulators. The identified modulators are
 CC useful as herbicides.
 CC
 XX
 SO Sequence 488 AA;
 Query Match 12.3%; Score 282; DB 23; Length 488;
 Best Local Similarity 26.8%; Pred. No. 1e-17;
 Matches 112; Conservative 60; Mismatches 158; Indels 88; Gaps 18;
 QY 37 ILTAGGLAPCNSAIGSLIERYTEIDPSIEIICRGQYKGLGDSYPYATVRKK 87
 DB 96 IYTCGGLCPGLNTVIREVSSLSYMGVRIIGIDVSL-----GGYRFYAKNTIPPLMS 149
 QY 88 EVRKAGVLQRFQGSVIGNSRVKLTNVKDCVVRGLVKEGEDPQKVAADQLVXGVDILHT 147
 DB 150 KY---VNDIHKRGQGTIIIGTSR-----GGHDTNKL-VDSIQDQNGINQVYI 189
 QY 148 IGGDDNTTAAADLAALFANNNGLTIVIGLPTVNDVPPFIKOSLGAWTAAGQARYFM 205
 DB 190 IGGDDTQKASVIFEEIRRLKAVAVGLPKTIIDNDIPYIDSFGDTVAEAGRAINAA 249
 QY 206 NYVAENANPEMLIVHEVWGNCGWLTAAOBYRKLDRAEMLPELGLTRSEYVAHVP 265
 DB 250 NYVAENANPEMLIVHEVWGNCGWLTAAOBYRKLDRAEMLPELGLTRSEYVAHVP 248
 QY 266 VPEMAIDLEAA-----KRLREVMKDCVNTIVSFGAGYEAIVAEKQAGQEVPPDA 318
 DB 289 IPSPSPYTLGEGGLFEFIRRLKDHGMV-----IVABAGQDLCKSKMES-----TPMDA 340
 QY 319 FGHIKLDAVNPGRKMGQEPQAMIGAEKTLVQ-----KSGYFARASASNVDMILIKSCADL 374

DB 341 SGRKLEKDY--GLWISQSIKDHFKNNKRWMTKYIDPTMIRAVPSNADNVYCTLLAQS 398
QY 375 AVECAFRRESGVIGHDED--NENVLRAIFEPRIKSGKPEINIDTD--WENSMLEIGQP 428
DB 399 AVHGAM--AGTGTGYSGLVNER-QTYIFRYRITERQNNVVTIDRMAR-LISSTNQP 451

RESULT 6
AAG39480
ID AAG39480 standard; Protein; 485 AA.
XX
AC AAG39480;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SBQ ID NO: 48654.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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PR 21-OCT-1999; 99US-0160815.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
Query Match 12.3%; Score 281.5; DB 21; Length 485;
Best Local Similarity 26.7%; Pred. No. 1,16-17;
Matches 109; Conservative 61; Mismatches 166; Indels 73; Gaps 16;
QY 37 ILTGGAGPACNSMIGSIRYETIDPSITICRYGKGLLDSPYTAERKAGV. 96
DB 96 IVTGGAGPACNSMIGSIRYETIDPSITICRYGKGLLDSPYTAERKAGV. 152

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QY 97 QRPQGSVYGNHRYKLTNNKDCYKGLVKEGEDPQKVAADQLYKQGVDIHTIGSDPTMFA 156
DB 153 HRRGGTITIGTSR-----GGHNTNFI-VDSIODRGINDQYITIGSGGTORG 195
QY 157 AADLAFLARNNYGLTVIGLPTVNDVDFPIKQSIGAWTAEOGARVF--NNVVAENNAN 214
DB 196 ASVIFEEIRRLRLKAVAVGIPKTIINDIPLVIDKSGPDTVAEAGRAIIVAAVEAESNN 255
QY 215 PMLIVHEVNGNCGMLTPATQSEYRKILDRAMPLEIGLTRESYEVAAVFPPEAIDIE 274
DB 256 GIGFV--KLNGRYSGVIA-----WYATLASADVDCCLPESPEYIE 294
QY 275 AEA-----KRLRMDKVDGCVNIFVSEGAQVFAIVEMQKQGEVPDRAHGIKLDAV 327
DB 295 GEGGLPEPFRRLKRLKHNV-----IVLAEAGQDLCKSMES---TPMDASGNLKHV 346
QY 328 NPKWPFGEQPAQMIGAEKTLVQ---KSGYPARASAVNDRLIKSCADLAVECAFRE 383
DB 347 --GLWLSQSIKDHFKKKNKVMMLKYIDPTYMIKRAVPASNDVYCTLLAQSAVHGAM--- 401
QY 384 SGVIGHDED--KGNVLAIEEPRIKSGKPFNIDTP--NFNSMLSEIGOP 428
DB 402 AGTGTSGLVNGR-QTYIPFRITETONNVVITDRPMAR-LLSSTNOF 448
RESULT 7
AAR71580
ID AAR71580 standard; Protein; 483 AA.
XX
AC AAR71580;
XX
DT 25-MAR-2003 (updated)
DT 11-OCT-1995 (first entry)
XX
DE Flavaria brownii fructose-6-phosphate 1-phosphotransferase.
XX
KW ATP-dependent fructose-6-phosphate 1-phosphotransferase enzyme; plant;
KW potato; Solanum tuberosum; rice; Oryza sativa; maize; Zea mays; radish;
KW Raphanus sativus; Flavaria brownii; primer; expression vector;
KW Agrobacterium tumefaciens; sugar; storage; temperature.
XX
OS Flavaria brownii.
XX
PN WO9505457-A1.
XX
PD 23-FEB-1995.
XX
PF 16-AUG-1994; 94WO-JP01352.
XX
PR 19-AUG-1993; 93JP-0226454.
XX
PA (NISR) JAPAN TOBACCO INC.
XX
PI Hiyoshi T, Kaseoka K, Mine T, Page MJ, Tyson HR;
DR WPI, 1995-098757/13.
DR N-PSDB; AA083963.
XX
PT DNA coding for fructose-6-phosphate 1-phosphotransferase - of
PT plant origin, for prodn. of transformant plant cells with altered
PT sugar content
XX
PS Claim 6; Page 39-43; 79pp; Japanese.
XX
CC The amino acid sequence of the novel ATP-dependent fructose-6-phosphate
CC 1-phosphotransferase enzyme (BC 2.7.1.11; PFK) encoded by the Flavaria
CC brownii gene PFK-FBI. Plants transformed with these genes can express
CC the enzyme. The transformed plants can produce varieties that have
CC altered sugar content on storage at low temperatures.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 483 AA;

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XX  Hiyoshi T, Kasaoka K, Mine T, Page MJA, Tyson HR;
XX  WPI; 1995-098757/13.
XX  N-PSDB; AAQ85986.
XX  DNA coding for fructose-6-phosphate 1-phosphotransferase - of
XX  plant origin, for prodn. of transformant plant cells with altered
XX  sugar content
XX  Claim 11; Page 58-61; 79pp; Japanese.
XX  The amino acid sequence of the novel ATP-dependent fructose-6-phosphate
XX  1-phosphotransferase enzyme (EC 2.7.1.11; PFK) encoded by the Raphanus
XX  sativus (radish) gene, pPFK-RS1. Plants transformed with genes encoding
XX  PFK (see AAQ85982-86) can express the enzyme. The transformed plants
XX  can produce varieties that have altered sugar content on storage at low
XX  temperatures.
XX  (Updated on 25-MAR-2003 to correct PN field.)
XX  SQ Sequence 426 AA;
XX  Query Match 11.5%; Score 263; DB 16; Length 426;
XX  Best Local Similarity 25.8%; Pred. No. 5.1e-16;
XX  Matches 108; Conservative 65; Mismatches 173; Indels 72; Gaps 17;
XX  37 ILTNGIAPCLNSAIGSLIERTEIDPSIEICRGYKGLLDSDYFVAVKKAQVL 96
XX  50 IVTGGIPLGNTVIRREIVCGISTVYGVKILGIBGIRGTYANTIDLDL--KTVNDI 106
XX  97 QRFGGSVIGNSRVKLTNVKDCVKRGLVYEGEDPQKVAADQLVKGVLDILHTIGDDTNTA 156
XX  107 HKRGITIGTSR-----GHDITTKI--VDSIQDRGINQVYIIGDGSQNG 149
XX  157 AADLAFLARNNYGLTVGLPKTVNDVFPFKQSGATTAABQGRFPMNVANANPR 216
XX  150 AAVFEIRRRGRLKVAAGIKPTIDNDIPIDRSFGDTVAEAKAIAAHVATSFEN 209
XX  217 MELIYHVMKNCGMILTAATQAEKRLDRAEMPELGLTRSEYVHVAFFEMADIEAB 276
XX  210 GIGLVKMKRYSGLPAM-----YARLASR-----DYDCLIPESFFLEGR 250
XX  277 -----AKRLRYNDKVDQCNITFVSGAGVBAIVAEQAKQGVPRDAGHITLDAVNP 329
XX  281 GGLFEFICKRLKEIGHNV-----IVLAGAG--QDLIAESNEQSTTL--KDAAGNKILQDV-- 302
XX  330 GKMPGEQGNMGIGAEKTLVQK--SGYFARASASNVDMRLIKSCADLAVECAFRRSSGV 386
XX  303 GLMISQRIKCHPAKKMTINLKYIDPTVITRAVPSNASD---NVCTTLAQSAVAH---GV 355
XX  387 I-GHDEDNQNVLRA-----IEPPRI--KSGKPFNIDTWMNSMLSEIQPKGKVAVSH 437
XX  356 MAGVNGFVGLVNGHTYIPYRIITEKQNKVITDRMAR--TLSTNQPSMKKDDHH 412
XX  RESULT 10
XX  ID AAR1579 standard; Protein; 485 AA.
XX  AAR1579;
XX  25-MAR-2003 (updated)
XX  11-OCT-1995 (first entry)
XX  Solanum tuberosum fructose-6-phosphate 1-phosphotransferase.
XX  ATP-dependent fructose-6-phosphate 1-phosphotransferase enzyme; plant;
XX  potato; Solanum tuberosum; rice; Oryza sativa; maize; Zea mays; radish;
XX  Raphanus sativus; Flaveria brownii; primer; expression vector;
XX  Agrobacterium tumefaciens; sugar; storage; temperature.
XX  Solanum tuberosum.
XX  OS
XX  XX

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PN  WO9505457-A1.
XX  23-FEB-1995.
XX  16-AUG-1994; 94WO-JP01352.
XX  19-AUG-1993; 93JP-0226454.
XX  (NISB ) JAPAN TOBACCO INC.
XX  Hiyoshi T, Kasaoka K, Mine T, Page MJA, Tyson HR;
XX  WPI; 1995-098757/13.
XX  N-PSDB; AAQ85982.
XX  DNA coding for fructose-6-phosphate 1-phosphotransferase - of
XX  plant origin, for prodn. of transformant plant cells with altered
XX  sugar content
XX  Claim 4; Page 33-37; 79pp; Japanese.
XX  The amino acid sequence of the novel ATP-dependent fructose-6-phosphate
XX  1-phosphotransferase enzyme (EC 2.7.1.11; PFK) encoded by the potato
XX  (Solanum tuberosum) gene pFK32. The DNA sequence was isolated from a
XX  potato cDNA library using primers AAQ85987-91. The sequence was used to
XX  construct the plant expression vector pPFK(35S) which was transformed
XX  into potato plants (Bintje variety) via Agrobacterium tumefaciens. The
XX  transformed plants can express the enzyme and produce plant varieties
XX  that have altered sugar content on storage at low temperatures.
XX  (Updated on 25-MAR-2003 to correct PN field.)
XX  SQ Sequence 485 AA;
XX  Query Match 11.5%; Score 262; DB 16; Length 485;
XX  Best Local Similarity 25.7%; Pred. No. 7.8e-16;
XX  Matches 113; Conservative 56; Mismatches 179; Indels 92; Gaps 17;
XX  7 YHITADIRCFHWFLENFNYITLNRKPKVAIITAGGIAPCLNSAIGSLIERTEIDPSIE 66
XX  86 YFSGDDVAC-----IVTCGLCPGLMTVIRREIVHSLDYMGVNK 125
XX  67 IICRGYKGLLDSDYFVAVKKAQVLQKSGSVIGNSRVKLTNVDCVARGLVKSG 126
XX  126 VFGIDGTYRFPYSKNTINILTP--KTVNDIHKRGITIGTSR-----GQ 166
XX  127 EDPQVAADQLVGDVLDILHTIGDDTNTAADLAFLARNNYGLTVGLPKTVNDVVP 186
XX  167 HDITTKI--VDSIQDRREINQVYIIGDGTQKGAIVYIEIRRRGLKTVAGIKPTIDNDIPV 225
XX  187 IKOSLGAMTAAGCAAFPMNVAVANNANPRMLIVHEVMKNCGMILTAATQAEKRLDRA 246
XX  226 IDRSFGDTVAEAKAIAAHVBAESANGVGVKIMRGYSGLFIA----- 271
XX  247 EMFLPGLTRSEYVHVAFFEMADIEABA-----KRLRYNDKVDQCNITFVSGAG 299
XX  272 -----MYATLASADVDLCLIPESFFLEBDGGLFEYIIRKLNKNGMV-----IVLAGAG 322
XX  300 VEAIVAE--NQAKQGVPRDAGHITKLDVAVNGKMPGEQGNMGIGAEKTLVQ-----KSG 352
XX  323 QDLIAESNEQSTTL--KDAAGNKILQDV--GLMISQRIKCHPAKKMTINLKYIDPT 376
XX  377 YMIRAVPSNASDN---VYCTTLAQSCVHAGMAGYTGFTSGLVNGR--QYIIPFRIITEKQV 432
XX  411 ENITD--WNSMLSEIQP 428
XX  433 MYVITDRMAR--TLSTNQPS 451
XX  RESULT 11
XX  ID ABB93109 standard; Protein; 500 AA.
XX  ABB93109

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XX	AB993109;
XX	
DT	31-MAY-2002 (first entry)
XX	
DE	Herbicidally active polypeptide SEQ ID NO 2320.
XX	
KW	Herbicidal; plant; agriculture; herbicide.
XX	
OS	Arabidopsis thaliana.
XX	
FN	WO200210210-A2.
XX	
PD	07-FEB-2002.
XX	
PF	28-AUG-2001; 2001WO-BP09892.
XX	
PR	28-AUG-2001; 2001WO-EP09892.
XX	
PA	(FARB) BAYER AG.
XX	
PI	Tietjen K, Weidler M;
XX	
DR	WPI; 2002-269010/31.
PT	
PT	Identifying plant target proteins for herbicidally active compounds,
PT	comprising aligning and comparing nucleic acid or amino acid sequences
PT	from plant with nucleic acid or amino acid sequences from non-plant
PT	organisms -
PS	Claim 5; SEQ ID NO 2320; 261pp + Sequence Listing; English.
XX	
CC	The invention relates to identifying target proteins
CC	(AB990790-AB994016) for herbicidally active compounds, comprising
CC	aligning and comparing nucleic acid or amino acid sequences from plant
CC	with nucleic acid or amino acid sequences from non-plant organisms using
CC	suitable search parameters, where plant sequences having an E-value
CC	greater by a factor of 3 than the E-value of most similar non-plant
CC	sequences are selected. The polypeptides or nucleic acids encoding them
CC	are useful as herbicides. The identified modulators are
CC	useful as herbicides.
SQ	Sequence 500 AA;
	Query Match 11.3%; Score 257.5; DB 23; Length 500;
	Best Local Similarity 25.6%; Pred. No. 2.2e-15;
	Matches 109; Conservative 59; Mismatches 167; Indels 91; Gaps 16;
OY	
DB	37 ILTAGGLAPCNSAIGSL-----IERTRYIDPSIEIIC-----YRGYKGLL 78
	: : :
OY	92 IVTGGGLPGANTVIREIVSSLSHYGVKRLIGDVS--FDCLLLTKNTNGSYRGEY 148
	: : :
OY	79 LGSYPVTAVERKKAGVLORFGGSVIGNSRVLTNNKDCVKRGLVKSGEDPKVAADOLV 138
	: :
DB	149 AKNTVSLDSKY--VMDIHKGKGTILGTSR-----GGHDTFKI-VDSIQ 188
	: : :
OY	139 KDGVDLITTTGGDDNTMTAAADLAFLANNVGLTYIGHPKTYNDNVFPKKSIGAMTAAE 198
	: : :
DB	189 DRGINQVYIIIGDGTOQRGAISVFEEIRRRGLKVAVIGIKTIIDNDIPVIDSFGDTAVE 248
	: : :
OY	199 QGARFYNNVVVNENNANPRMLIVHEWGGRNCGLMTATATQEVKRKLIDRAEWLPGLITRES 258
	: : :
DB	249 EAQRALNAHAWEAESIEINGIVVVKLMGRYSGRFA-----MYATLAS 289
	: : :
OY	259 YEYHAVFFPEMAIDLEAE-----KELREVMKDYCCNIIFVSGAGVEALVALMOAKG 311
	: : :
DB	290 RDVDCCLIPESPFYIEGGEGGLEFEYTEKRLKESGHNV---LVIAAGAAGDLMSSKSMEM- 344
	: : :
OY	312 QEVPDAIAGHILDAVNEPKWFGEQFAQMIGAETLVQ----KSGYFARASASNVDNRL 367
	: : :
DB	345 --TLSDASGNKLLKDV--GLMWSQSIKHFNQKKRWVNLKIYDPYIMIRAVPSNASDNVY 400
	: : :
OY	368 IKSCADLAVECAFRESGYIEDHDONGNV--LRALIEPRRIKGGKPPFIIDD--WFSNML 422

Db	401	CTLL6SAVHGAMAGTGYI-----SGLVNGRQTYIFPYRITERKQNHVITDRMAR-LL 454
Qy	423	SEIGOP 428
Db	455	SSTNOP 460
RESULT 12		
ID	AA636438	
ID	AA636438	standard; Protein; 473 AA.
XX	AA636438;	
AC		
XX		
DT	18-OCT-2000	(first entry)
XX		
De	Arabidopsis thaliana	protein fragment SEQ ID NO: 44655.
XX		
Kw	Protein identification; signal transduction pathway; metabolic pathway;	
Kw	hybridisation assay; genetic mapping; gene expression control; promoter;	
Xw	termination sequence.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	BP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PP	25-FEB-2000; 2000EP-0301439.	
XX		
PR	25-FEB-1999;	99US-0121825.
PR	05-MAR-1999;	99US-0123180.
PR	09-MAR-1999;	99US-0123548.
PR	23-MAR-1999;	99US-0125788.
PR	25-MAR-1999;	99US-0126264.
PR	29-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
PR	06-APR-1999;	99US-0128234.
PR	08-APR-1999;	99US-0128714.
PR	16-APR-1999;	99US-0129845.
PR	19-APR-1999;	99US-0130077.
PR	21-APR-1999;	99US-0130449.
PR	23-APR-1999;	99US-0130510.
PR	23-APR-1999;	99US-0130891.
PR	28-APR-1999;	99US-0131449.
PR	30-APR-1999;	99US-0132048.
PR	30-APR-1999;	99US-0132407.
PR	04-MAY-1999;	99US-0132484.
PR	05-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132486.
PR	07-MAY-1999;	99US-0132487.
PR	11-MAY-1999;	99US-0134256.
PR	14-MAY-1999;	99US-0134218.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
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 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

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 Best local Similarity 25.2%; Pred. No. 8, 2e-15;
 Matches 103; Conservative 60; Mismatches 174; Indels 72; Gaps 15;

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 DB 97 ITCGGICPGELNTRIVREIVICGSLYGVRRILGIDGVRGFAARNTHIDL--KTVNDI 153

QY 97 QRFSSVIGNSRKYLTINVKOCVKEGLVKEGEDPOKVAADQVVDVLIHTIGDDDTNTA 156
 Db 154 HRSGGTILIGTSR-----GGHNTTKI-VDSIDQRGINQVYIIGDSSQKG 196
 QY 157 AADLAFLARNNGYGLTVIGLPTVDNDVFPKISLGAMTAAGQAFYFNNVVAENNANPR 216
 Db 197 AAALFEIRKRLKLVAVAGIPKTIIDNDIPIDRSFGPDVAEQAQAINAAHFAEASFEN 256
 QY 217 MLIVHEVNGRNGCMLTAAQAEYRKLDRAEMLPELIGLTRESYEVHAFVPEKADILEAE 276
 Db 257 GIGLVKLMGRYSGFIA-----MHATLASRDVDCCLIPESPFLEBS 297
 QY 277 A-----KRLREVMKVCVNI FVSEGAVEAIVAEQAGQVPRDAPGHKLDVNP 329
 Db 298 GGLFEPIDKRLKESGHN-----IVIAEGAGDILSESM--KESTTLKDSAGNKLQDI-- 349
 QY 330 GKMFGEQFAOMIGAEKTLVQK--SGYFAPASASNVDDWRLIKSCADLAVECAFRESGV 386
 Db 350 GLWISQRIKDHFAKQWTLTKYIDPTYMIKRAVPSNAD---NVCTTLAQSAVH--GV 402
 QY 387 I-GHEDENGVLR-----IEPPI--KGKPNIDTDWNSMLSEIGOP 428
 Db 403 MAGYNGFTVGLVNGRHTYIPFNRIKONKVVITDRMAR-LISSTNOP 450

RESULT 13

ABB93145
 ID ABB93145 standard; Protein: 473 AA.

AC ABB93145;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 2356.

XX Herbicidal; plant; agriculture; herbicide.

XX Arabidopsis thaliana.

XX WO200210210-A2.

XX 07-FEB-2002.

XX 28-AUG-2001; 2001WO-EP09892.

XX 28-AUG-2001; 2001WO-EP09892.

XX (FARB) BAYER AG.

XX Tietjen K, Weidler M;

XX WPI; 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds.

PT comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant

PT organisms.

XX Claim 5; SEQ ID NO 2356; 261bp + Sequence Listing; English.

XX The invention relates to identifying target proteins

CC (ABB90790-ABB94016) for herbicidally active compounds, comprising

CC aligning and comparing nucleic acid or amino acid sequences from plant

CC with nucleic acid or amino acid sequences from non-plant organisms using

CC suitable search parameters, where plant sequences having an E-value

CC greater by a factor of 3 than the E-value of most similar non-plant

CC sequences are selected. The polypeptides or nucleic acids encoding them

CC are useful for herbicides. The identified modulators are

CC useful as herbicides.

Best Local Similarity 25.2%; Pred. No. 8,2e-15;
 Matches 103; Conservative 60; Mismatches 174; Indels 72; Gaps 15;

QY 37 ILTAGGLADCLNSALIGSLIERYTEIDPSIEIICYRGYGLLIGDSYPYAEVRKZAGYL 96
 Db 97 IYVGGCLGLMTVIEIYIGSLSYWGVKRIIGIDGYSGFARNTHIDL--KTVNDI 153
 QY 97 QRFSSVIGNSRKYLTINVKOCVKEGLVKEGEDPOKVAADQVVDVLIHTIGDDDTNTA 156
 Db 154 HRSGGTILIGTSR-----GGHNTTKI-VDSIDQRGINQVYIIGDSSQKG 196
 QY 157 AADLAFLARNNGYGLTVIGLPTVDNDVFPKISLGAMTAAGQAFYFNNVVAENNANPR 216
 Db 197 AAALFEIRKRLKLVAVAGIPKTIIDNDIPIDRSFGPDVAEQAQAINAAHFAEASFEN 256
 QY 217 MLIVHEVNGRNGCMLTAAQAEYRKLDRAEMLPELIGLTRESYEVHAFVPEKADILEAE 276
 Db 257 GIGLVKLMGRYSGFIA-----MHATLASRDVDCCLIPESPFLEBS 297
 QY 277 A-----KRLREVMKVCVNI FVSEGAVEAIVAEQAGQVPRDAPGHKLDVNP 329
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 QY 330 GKMFGEQFAOMIGAEKTLVQK--SGYFAPASASNVDDWRLIKSCADLAVECAFRESGV 386
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 QY 387 I-GHEDENGVLR-----IEPPI--KGKPNIDTDWNSMLSEIGOP 428
 Db 403 MAGYNGFTVGLVNGRHTYIPFNRIKONKVVITDRMAR-LISSTNOP 450

RESULT 14

AA36437
 ID AA36437 standard; Protein: 537 AA.

AC AA36437;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 44654.

XX Protein identification; signal transduction pathway; metabolic pathway;

XX hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

XX Arabidopsis thaliana.

XX EP103405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 23-APR-1999; 99US-0130891.

XX 28-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 30-APR-1999; 99US-0132407.

XX 04-MAY-1999; 99US-0132484.

XX 05-MAY-1999; 99US-0132485.

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Query Match 11.0%; Score 251; DB 21; Length 537;
Best Local Similarity 25.2%; Pred. No. 9, 9e-15;
Matches 103; Conservative 60; Mismatches 174; Indels 72; Gaps 15;

QY 37 ILTAGLAPLNSAIGSLIERTIDPSLEIICRGYIGLLGDSYPTAEVRKAGVL 96
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QY 97 QRFSGSVIGNSRFKLTNVKDCVRKGLKEGDEPKVAADQLVQGVDLFTIGDDTNTA 156
DB 218 HRSGGIIIGSR-----GSHHTTKI-VDSIQDRGINOYIIIGDGSQNG 260
QY 157 AADLAAFLARNNGYLTIVGLPTVDNDVPIKQSLGAWTAAGAAEFYFNNVVAENANER 216
DB 261 AAALFEIRKRLKLVAVAGIPKTIIDNDIPIIDRSFGPDRAVBAQAIANAHEATSFEN 320
QY 217 KLIIVHEMRNCGMLAATAQAEKRLDAAEMLPGLTRESVEVAIVPEMAIDLEAE 276
DB 321 GGLVTKMRYSFFIA-----MHATLASIDVCCILPSPPTLBSG 361
QY 277 A-----KRLBEWMDKVCNIFVSEGAVEAIVEMQAKGEVPRDAFGHIKLDANVP 329
DB 362 GGLFERIDRLKESGHV-----IVIAEGAGDPLSESM--KESITLTKDASGNKLLQDI-- 413
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DB 414 GMSISRIQIDHPAKKWTLLTKTIDPTMTLRAVPSNASD---NVCTLLAQSAVH--GV 466
QY 387 I-GHEDNGNVLAA-----IEFPRI--KGKXPNIIDTFNMSLSEIGP 428
DB 467 MAGYNGFTGLVNGRHTYIPFNRIITEKQKXVITDRMAR-ILSSTNCP 514

RESULT 15
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ID AAG39481 standard; Protein, 366 AA.
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AC AAG39481;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48855.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.

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 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 16-OCT-1999; 99US-0159584.
 PR 16-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 25-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 10.8%; Score 247; DB 21; Length 366;
 Best Local Similarity 26.1%; Pred. No. 1.3e-14;
 Matches 102; Conservative 56; Mismatches 151; Indels 82; Gaps 17;

QY 55 IERYTEIDPSIEHICRGYKGLLDGSPVPAEVRKKAQVLPFGSGVYGNRVLTVV 114
 DB 4 VKRIILGID-----GGRGFYAKNTIFPNSKV---VNDIHKRGITIGISR----- 45
 QY 115 KDCVKEGLVKEGDEPOKVAADQIVKQGVDIEMHTIGDDDTNTAAADIAFLARNNGLYI 174
 DB 46 -----GGHDTMKI-VDSIQDRGINQVYIIIGDGTORGASVIFEBIRRRRLKVAUV 94
 QY 175 GLPKYDNDVFPFKOSIGAMTAEGGARYF--MNVVAENNANPRKLIHEVMGRNCGMLT 232
 DB 95 GIPKTIIDNDIPVLDKFGPDIAVEBQRAINAAHVEBSNENSGIFV--KLMGRYGYIA 152
 QY 233 AATRAOERYKLDRAEWLPEIGLTFRESYEVHAFVPEMAIDLEAA-----XRLREVM 285
 DB 153 -----MYATIASRDVDCCLIPESPYLEEGGLFEFIERRLDHGH 193
 QY 286 KUDCNMIIFNSEGAGVLAIVAEKQAGQVPRDAPGHIXLDAYVPGKPFQPMGABK 345
 DB 194 MV-----IVLABGQGLMKCSMES---TPMDSSGNKLNDV--GLMISGTDHTRKNK 243
 QY 346 TLVQ-----KSGYFARASASNVDMRLIKSCADIAVECAPRRESGVGHDED--NGVTLRA 399
 DB 244 MWNLIKIDPTVMIRAVPSNASDNVCTLLAGAAVHAM---AGYGYTSGLVNGR-QTY 289
 QY 400 IEPRIKGGKPRNIDT--WPNMSEIGOP 428
 DB 300 IPEYRIETQNNVVTIDRMVAR-LISSTNOP 329

Search completed: January 29, 2004, 14:36:32
 Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 14:35:42 : Search time 21 Seconds
(without alignments)
880.469 Million cell updates/sec

Title: US-09-941-947a-2
Perfect score: 2284
Sequence: 1 DVTWTPYHLTDIRFCHEMF.....FNSMLSEIGQPKGKVEVSH 437

Scoring table: BLOSUM62
Gapco 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/aa/5B.COMB.pep:*
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4: /cgn2_6/prodata/1/aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/aa/6C.COMB.pep:*
6: /cgn2_6/prodata/1/aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2284	100.0	437	US-09-934-901-16 Sequence 16, Appl
2	270	11.8	483	US-08-416-870C-4 Sequence 4, Appl
3	264.5	11.6	469	US-08-416-870C-6 Sequence 6, Appl
4	262	11.5	485	US-08-416-870C-2 Sequence 2, Appl
5	260	11.4	426	US-08-416-870C-10 Sequence 10, Appl
6	226.5	9.9	345	US-09-134-001C-3774 Sequence 3774, Ap
7	215.5	9.4	323	US-09-107-532A-6470 Sequence 6470, Ap
8	211.5	9.3	522	US-08-416-870C-8 Sequence 8, Appl
9	206.5	9.0	781	US-08-280-690-2 Sequence 2, Appl
10	181	7.9	550	US-09-198-452A-225 Sequence 225, App
11	171.5	7.5	544	US-09-198-452A-180 Sequence 180, App
12	113.5	5.0	845	US-09-198-452A-458 Sequence 458, App
13	99.5	4.4	1038	US-09-541-782-4 Sequence 4, Appl
14	99.5	4.4	1038	US-09-723-820-4 Sequence 4, Appl
15	96	4.2	863	US-09-328-352-6730 Sequence 6730, Ap
16	95.5	4.2	412	US-09-252-991A-30252 Sequence 30252, A
17	94.5	4.1	572	US-09-702-705-1815 Sequence 1815, Ap
18	94.5	4.1	572	US-09-736-457-1815 Sequence 1815, Ap
19	94.5	4.1	646	US-09-328-352-6017 Sequence 6017, Ap
20	94	4.1	546	US-09-252-991A-22048 Sequence 22048, A
21	94	4.1	641	US-09-613-303-51 Sequence 51, Appl
22	94	4.1	670	US-09-852-991A-26867 Sequence 26867, A
23	93.5	4.1	4	US-09-328-352-5684 Sequence 5684, Ap
24	93.5	4.1	503	US-07-612-673-2 Sequence 2, Appl
25	93.5	4.1	521	US-07-796-361A-11 Sequence 11, Appl
26	93.5	4.1	521	US-08-539-666-2 Sequence 2, Appl
27	93.5	4.1	690	US-09-252-991A-32350 Sequence 32350, A

28	93.5	4.1	789	US-09-107-532A-6734 Sequence 6734, Ap
29	93.5	4.1	5087	US-09-144-085-1 Sequence 1, Appl
30	93	4.1	523	US-08-997-080-114 Sequence 114, App
31	93	4.1	523	US-08-997-362-114 Sequence 114, App
32	93	4.1	523	US-09-095-855-114 Sequence 114, App
33	93	4.1	523	US-09-324-542-114 Sequence 114, App
34	93	4.1	523	US-09-205-426-114 Sequence 114, App
35	93	4.1	541	US-08-997-080-160 Sequence 160, App
36	93	4.1	541	US-08-997-362-160 Sequence 160, App
37	93	4.1	541	US-09-095-855-160 Sequence 160, App
38	93	4.1	541	US-09-324-542-160 Sequence 160, App
39	93	4.1	541	US-09-205-426-160 Sequence 160, App
40	93	4.1	682	US-09-252-991A-31275 Sequence 31275, A
41	93	4.1	2411	US-09-268-347-36 Sequence 36, Appl
42	92.5	4.0	215	US-08-997-080-117 Sequence 117, App
43	92.5	4.0	215	US-08-997-362-117 Sequence 117, App
44	92.5	4.0	215	US-09-095-855-117 Sequence 117, App
45	92.5	4.0	215	US-09-324-542-117 Sequence 117, App

ALIGNMENTS

RESULT 1
US-09-934-901-16
Sequence 16, Application US/09934901
Patent No. 6555353
GENERAL INFORMATION:
APPLICANT: Odom, J. Martin
APPLICANT: Koffas, Matheos
APPLICANT: No. 6555353ton, Kelley C.
APPLICANT: Ye, Rick
TITLE OF INVENTION: IDENTIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: C1619 US NA
CURRENT FILING DATE: 2001-08-22
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/223,906
PRIOR FILING DATE: September 1, 2000
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Office 97
SEQ ID NO 16
LENGTH: 437
TYPE: PRT
ORGANISM: METHYLOMONAS SP.
US-09-934-901-16

Query Match	100.0%	Score 2284	DB 4	Length 437
Best Local Similarity	100.0%	Pred. No. 3.8e-216		
Matches 437	Conservative 0	Mismatches 0	Indels 0	Gaps 0
1	DVTWTPYHLTDIRFCHEMFLENFYTLNKKPKVAITAGLAPCTNSAIGSLIBRYTE	60		
1	DVTWTPYHLTDIRFCHEMFLENFYTLNKKPKVAITAGLAPCTNSAIGSLIBRYTE	60		
61	IDPSIEIICVNGYKGLLEDSPYTAERKKAQVORFGGSVIGNSRVKLTNVKDCYKR	120		
61	IDPSIEIICVNGYKGLLEDSPYTAERKKAQVORFGGSVIGNSRVKLTNVKDCYKR	120		
121	GLVYEGDPOKVAADQVYKGVVDILHTTIGDDNTTAADLAFLANNNYGLTVGLPPTV	180		
121	GLVYEGDPOKVAADQVYKGVVDILHTTIGDDNTTAADLAFLANNNYGLTVGLPPTV	180		
181	DNDVFPKOSIGANTAAOGARFYNNVAENNNAPRLIYIEVWGRNCGMLTAATAQRYR	240		
181	DNDVFPKOSIGANTAAOGARFYNNVAENNNAPRLIYIEVWGRNCGMLTAATAQRYR	240		
241	KLDRAEMLPELGLTRSYEYHAFAVPEKALIDAEAKRLREWDKDCVNI FVSEAGV	300		
241	KLDRAEMLPELGLTRSYEYHAFAVPEKALIDAEAKRLREWDKDCVNI FVSEAGV	300		
301	EATVAEQAKQOEVPRAFGHITKLDVAVNPGKMFGEQFAQMGIAEKLTVOKSGYFARASAS	360		
301	EATVAEQAKQOEVPRAFGHITKLDVAVNPGKMFGEQFAQMGIAEKLTVOKSGYFARASAS	360		

QY 361 NVDDMRILKSCADIAVECAFRRSGVIGHDEDNQVLAIEFPRIKGGKPNIDTWENS 420
 DB 361 NVDDMRILKSCADIAVECAFRRSGVIGHDEDNQVLAIEFPRIKGGKPNIDTWENS 420
 QY 421 MLSTIGQPKGKGVESH 437
 DB 421 MLSTIGQPKGKGVESH 437

RESULT 2
 US-08-416-870C-4
 Sequence 4, Application US/08416870C
 Patent No. 5824862

GENERAL INFORMATION:
 APPLICANT: HIYOSHI, TORU
 APPLICANT: MINE, TOSHIKI
 APPLICANT: KASAKA, KEISUKE
 APPLICANT: TYSON, ROBERT HUM
 APPLICANT: PAGE, ANTHONY MILES JOHN
 TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
 TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECT
 TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UND
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
 STREET: PO BOX 747
 CITY: FALL CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/416,870C
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY JR, GERALD M
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 760-195P(PCT)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 483 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-416-870C-4

Query Match 11.8%; Score 270; DB 2; Length 483;
 Best Local Similarity 27.6%; Pred. No. 5,6e-18;
 Matches 113; Conservative 53; Mismatches 175; Indels 68; Gaps 15;
 QY 36 ALITAGGLAPCLNSAGLSIERYTEIDPSIRICRGYKGLLDGSDYPTVAEVRKAGV 95
 DB 95 ALITAGGLAPCLNSAGLSIERYTEIDPSIRICRGYKGLLDGSDYPTVAEVRKAGV 95
 QY 95 ALITAGGLAPCLNSAGLSIERYTEIDPSIRICRGYKGLLDGSDYPTVAEVRKAGV 95
 DB 152 IHKRGITLIGSR-----GGHDKPKI-VDSIQRGINQVYIIGSDGTOK 194
 QY 152 IHKRGITLIGSR-----GGHDKPKI-VDSIQRGINQVYIIGSDGTOK 194
 DB 156 AAADLAATLARNRYLTIGLFTKTDNDVFPPIKOSLGATTAAGCARFNNVANNANP 215
 QY 156 AAADLAATLARNRYLTIGLFTKTDNDVFPPIKOSLGATTAAGCARFNNVANNANP 215
 DB 195 GAAYIVQEVRRGLKAVVAGIPIKTDNDIPEYIDKSFGEFTAVEAQRANAAHVEASAE 254
 QY 195 GAAYIVQEVRRGLKAVVAGIPIKTDNDIPEYIDKSFGEFTAVEAQRANAAHVEASAE 254
 DB 216 RMLIVHEVWGRNGMLTATATQEVYKLLDRAEMLPELGLTRSEYEVHAFVPEMAIDLEA 275
 QY 216 RMLIVHEVWGRNGMLTATATQEVYKLLDRAEMLPELGLTRSEYEVHAFVPEMAIDLEA 275

DB 255 NGIGVVKLMGRISGFLA-----MYATLASRDVDCIIPESPYYLG 295
 QY 276 EA-----KSLTEVNDKVCNIFVSBAGVYEAIVAENQAKQEVPRPAFGHIKLDAYN 328
 DB 296 EGGLEIYVEKRLDDGHW-----IYVABEGAGGELAAENLKT--TSTAKASGRKLLHDV- 348
 QY 329 PKRMFGBO-----PAQMGAKTIVQ-KSGYFAPASASNDMDRLIKSCADIAVECAFRR 383
 DB 349 -GLMISDKIKRHFAPKIPMEITLTKYIDPYMIRAVPSNASDN--VYCTLLAQSCVHGV 404
 QY 384 SGVIGHDED--NGNVLAIEFPRIKGGKPNIDTD--WFNSMLSEIGOP 428
 DB 405 AGTGTFTSLGVNKR-QTYIFPNRITKKNVVITDDMMAR-LLSTINOP 451

RESULT 3
 US-08-416-870C-6
 Sequence 6, Application US/08416870C
 Patent No. 5824862

GENERAL INFORMATION:
 APPLICANT: HIYOSHI, TORU
 APPLICANT: MINE, TOSHIKI
 APPLICANT: KASAKA, KEISUKE
 APPLICANT: TYSON, ROBERT HUM
 APPLICANT: PAGE, ANTHONY MILES JOHN
 TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
 TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECT
 TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UND
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
 STREET: PO BOX 747
 CITY: FALL CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/416,870C
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY JR, GERALD M
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 760-195P(PCT)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 469 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-416-870C-6

Query Match 11.6%; Score 264.5; DB 2; Length 469;
 Best Local Similarity 26.8%; Pred. No. 1.9e-17;
 Matches 109; Conservative 56; Mismatches 173; Indels 69; Gaps 16;
 QY 37 ILTAGGLAPCLNSAGLSIERYTEIDPSIRICRGYKGLLDGSDYPTVAEVRKAGV 96
 DB 74 IITAGGLAPCLNSAGLSIERYTEIDPSIRICRGYKGLLDGSDYPTVAEVRKAGV 96
 QY 97 QREGSVYIGSRKLTNNVNDQVKGGLVKEGSDPOQYAAADLVNDQVLDIHTIGSDDTNTA 156
 DB 131 HKRGGVLTGSR-----GGHDKPKI-VDSIQRGINQVYIIGSDGTORG 173
 QY 157 AAADLAATLARNRYLTIGLFTKTDNDVFPPIKOSLGATTAAGCARFNNVANNANP 216
 DB 157 AAADLAATLARNRYLTIGLFTKTDNDVFPPIKOSLGATTAAGCARFNNVANNANP 216

Db 174 AGVIFERIRRGKLVAVAGIPRTIDNDIPVLDSPFGDFAVEBAQRIANAAYEASAAEN 233
 Qy 217 MLIVHEMNGNGMIFPAATQAEKRLIDRAEMLPBGLTSEYVNAVFPPEMAIDLEAE 276
 Db 234 GIGLVKLNHSGTIA-----HATLASR-----DVDCCLPESPYLEGEH 274
 Qy 277 A-----KELREYMDKVCVNI FVSEGAVEAI VAEQAKGOEVPDAPGH-IXLDAVN 328
 Db 275 GGLFRLYEKLEKENGHNV-----IVVAGAGQKLIINTEKSMG-----KDSGNSILDDV-- 324
 Qy 329 PGRKFGQEPKMTGAKETLVQ---KSGYPARASASVNDMLIKSCADLAVECARRES 384
 Db 325 -GLMISQKIREHFKIKITTLNKXIDPTMIRAI PSNASDNVYCTLLAHRVAGAGAGYT 383
 Qy 385 G-VIGHEDNGNVLRAIEPPRI--KSGKPFNIDTWNMSLSEIGOP 428
 Db 384 GFTVVG--QVNGRHC-VIFPYRIEKKQKVSITDRMAR-LISSTNQP 426

RESULT 4
 US-08-416-870C-2
 ; Sequence 2, Application US/08416870C
 ; Patent No. 5824862

GENERAL INFORMATION:
 APPLICANT: HIYOSHI, TORU
 APPLICANT: MINE, TOSHIKI
 APPLICANT: KASAKA, KEISUKE
 APPLICANT: TYSON, ROBERT HUM
 APPLICANT: PAGE, ANTHONY MILES JOHN
 TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
 TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTO
 TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDE
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
 STREET: PO BOX 747
 CITY: FALL CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/416,870C
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY JR, GERALD M
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 760-195P (PCT)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 485 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-416-870C-2

Query Match 11.5%; Score 262; DB 2; Length 485;
 Best Local Similarity 25.7%; Pred. No. 3.4e-17; Index 92; Gaps 17;
 Matches 113; Conservative 56; Mismatches 179;
 Qy 7 YHLTADIRFGHFWPLNPFYTLNKKPKVAILTAGLIAPCLNSAGSLIRRYTEIDPSIE 66
 Db 86 YFSSDDVRAE-----IVTGGGLCPGLNTVIREIVHSLDVMYGVNK 125

Qy 67 IICVGGYKGLLIGDSYPTAEVERKAGYLORFGSSVIGNSRVKLTNNKDCVKGIVGE 126
 Db 126 VFGIDGGRGFGYFSKNIMILTP---KTVNDIHRGGTILGSSR-----CG 166
 Qy 127 EDPQKAAADQVKDGVDLHTIGEDDTFAADLAFLARNNYGLTVGLPKTVNDVPE 186
 Db 167 HPTTXI-VDSIQRIRINQYIIIGDGTQGAIVIEEIRRLKVIAGIPTITDNDIPV 225
 Qy 187 IKOSIGAMTAEGQARYEPQVVAENNANPRMLIVHEWGRNGMTLTAATQAEKRLIDRA 246
 Db 226 IKSFGFDVAEBAQRIANAAYEASAAENGVKMGVKKMGYSGFIA----- 271
 Qy 247 EMLPELGLTRESYEVNAVFPPEMAIDLEAE-----KELREYMDKVCVNI FVSEGA 299
 Db 272 -----MYATLASRDVLCILPESPYLEGDGGLFEYIERKLENGHNV-----IVVAGAG 322
 Qy 300 VEAIIVAE--MQAKGOEVPDAPGHIXLDAVNPGRKFGEOPAQMGAKETLVQ-----KSG 352
 Db 323 QELIABENNAHQEQ---DASGNKLLQDV--GLMISQKIRDF-ATKTMPTITLKIDPT 376
 Qy 353 YPARASASVNDMLIKSCADLAVECARRESGVIQHDG--NGNVLRAIEPPRIKGRP 410
 Db 377 YMIRAVPSNASDN---VYCTLLAQSCVHGAAGYGTGSLVNGR-QTVIPIPRITREKQ 432
 Qy 411 FNIDTD--WFNSMLSEIGOP 428
 Db 433 KVVITDRMAR-LISSTNQP 451

RESULT 5
 US-08-416-870C-10
 ; Sequence 10, Application US/08416870C
 ; Patent No. 5824862

GENERAL INFORMATION:
 APPLICANT: HIYOSHI, TORU
 APPLICANT: MINE, TOSHIKI
 APPLICANT: KASAKA, KEISUKE
 APPLICANT: TYSON, ROBERT HUM
 APPLICANT: PAGE, ANTHONY MILES JOHN
 TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
 TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTO
 TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDE
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
 STREET: PO BOX 747
 CITY: FALL CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/416,870C
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY JR, GERALD M
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 760-195P (PCT)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 426 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-416-870C-10

Query Match 11.4%; Score 260; DB 2; Length 426;
 Best Local Similarity 25.6%; Pred. No. 4.4e-17;
 Matches 107; Conservative 65; Mismatches 174; Indels 72; Gaps 16;

37 ILTAGLAPCLNSAIGSLIERYTEIDPSIEIICRGYKGLLDGSDPVTAEVKAGVL 96
 50 IVTCGGLCPGINTVIREIVCGLSYMGVYKILIEGGGREGFARANTDLDL---KTVNDI 106
 97 QRFSGVIGSRVYKLTNKKDCVCKGLVKEGEDPQVADOLVKDQVILHTIGDDTNTA 156
 107 HKRGSTILGSTR-----GGDDTTKI-VDSIQDGINQVITIGDSQKG 149
 157 AADLAFLARNNGVLTGPKTYDNDVFPKQSLGAWTAEGARFPMVAENMANPR 216
 150 AAVIFEEIRRRGKVAVAGIKPIDNDIPIDRSFGPDVAEAKAINAHVATSPEN 209
 217 MLIVHEVNGRCGWLTAATAGYEKKLDRAEWLDELITRESYEVHAFVPEMAIDLEAE 276
 210 GIGLVKELGRYSGLFA-----MATLASRDVDCCLIPESFPFLGK 250
 277 -----AKRLREVNDKVCNIFVSBGAGVEAIVAEQAGQEVPRDAGHINKLDAVNP 329
 251 GGLFEPICKRLKEIGHNV---IVYABAG-QDLASGNEGSTTL-KDASGNKLQGV-- 302
 330 GKATGEGQFQMTGAEKTVLQK---SGFPAASASNVDMRLKSCADLAVECAFRESGV 386
 303 GLMTSQRLKHFAKMTMLNLYIDETVMIRAVPSNASD---NVCCTLAQSAVH---GV 355
 387 I-GHEDENGVTLRA---IEPPRI--KGKGFENIDTWMFNSMLSEIGCPKQKGVESH 437
 356 MAGINGFTVGLVNGRHITIPFRIITEKONKVVITDRMAR-LISSTNQPSMKDDHH 412

RESULT 6
 US-09-134-001C-3774
 Sequence 3774, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 3774
 LENGTH: 345
 TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-3774

Query Match 9.9%; Score 226.5; DB 4; Length 345;
 Best Local Similarity 25.4%; Pred. No. 5.3e-14;
 Matches 105; Conservative 68; Mismatches 136; Indels 105; Gaps 19;

26 YTLNKKPKKVALITAGLAPCLNSAIGSLIERYTEIDPSIEIICRGYKGLLDGSDPV 85
 21 YVVM---KKIAYLISGSGSPGEMAAVRAVTR--TAIYNNIEVGVYGGYGLDDDDHKL 75
 86 TAEVKKAGVLRQFSGSVIGSRVYLTNVKDCVKGGLVKEGEDPQVADOLVKDQVIL 145
 76 --ELGSGVDITQR-GGTFLFSAR-----CPQ---FKE-EDVRKKAILEMLRRGIGL 120
 146 HTIGGDDTNTAADIAPLARNNTGLTIGPKTYDNDVFPKQSLGAWTAEGARFPMVAENMANPR 205
 121 VVIGDGSYRGAGQISEBCKE---IQTIIGPTIDNDINGTIDTIGFIDA-----L 168
 206 NVVAEN-----NANRMLIVHEVNGRCGWLTAATAGYEKKLDRAEWLDELITRES 257

169 NTIIEVDKIRDTASSHARTFIV-EVWMDCG-----DLALW---AGI----- 207
 258 SYEVHAFVPEMAIDLEAEKRLREVNDKVCNIFVSBGAGVEAIVAEQAGQEVPRD 317
 208 SVAGETIVPEVNTDVKDAKEIGQIKGKXHSI-----VVAESGMSGGCCAD 258
 318 AFCHIKLDAVNPQKMGEGQFQMTGAEKTVLQKSGFPAASASNVDMRLKSCADLAVE 377
 259 LTKYINID-----TRVSLGSHIQGGSGPSGADRYLASRLGAYAVE 298
 378 CAFRES-----GVIGHDENGVTLRAIEPPRI-KGKGFENIDTWMFNSMLSEIGC 427
 299 LKQGTANGVGI-----RNNQVLTSPDEI-----FAESDRKFNQMTLAK 341

RESULT 7
 US-09-107-532A-6470
 Sequence 6470, Application US/09107532A
 Patent No. 6583275
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSER: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Atinello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 6470:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 323 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc. feature
 LOCATION: (B) LOCATION 1...323
 SEQUENCE DESCRIPTION: SEQ ID NO: 6470:
 US-09-107-532A-6470

Query Match 9.4%; Score 215.5; DB 4; Length 323;
 Best Local Similarity 24.4%; Pred. No. 6.9e-13;
 Matches 94; Conservative 56; Mismatches 114; Indels 121; Gaps 17;

33 KKVAILTAGLAPCLNSAIGSLIERYTEIDPSIEIICRGYKGLLDGSDPVTAEVRK 92

Db 5 KRIGILTSGDAPGMAAFAVVR-----KGIYGL-----EV 37
 QY 93 AGYLORFGGSGVGN-SRUKLTINVKDCVKG-----LVKGEDEPOKVAADOLVR 139
 Db 38 YGINGFAGIAGADIRLDAVDGDKIQFGSTFLYSARYPEPATEEG---QLNGISQLKK 94
 QY 140 DGVDLHTTGGDDNTTAADLAFLANNVGLTVIGPKVNDVPPFKISLGANTRAEQ 139
 Db 95 FGIJGLVVIQGDSSYHGA-----MALTKRGPFAVGIPTGIDNDIPDTDFTIGFDTA--- 145
 QY 200 GAEFNNVAEN-----NANPRLIVHEVGRNCGMLTAATAOEYRKLDRAMELPE 251
 Db 146 -----INTVESIDRIKIDTATSHRTFVI-EVMGRNAG-----DIALMSGV 185
 QY 252 LGLTRESEYHAAVFPEPMAIDLEAAKRLFEVMD--KDCVNI FVSBGAVEAIVAEWQA 309
 Db 186 AGGADG-----IIPHPDPMASVAKKIQEGRDRGKGL-TILEG----- 226
 QY 310 KGGVPRPADFGHFKLDVNPGRKMGEGEQAQMGAKTLYQSGVFAPASAVNDKRLIK 369
 Db 227 -----VMGNEPAEGLSS-PQDYHTRVSLGHVYRGAAPSARDVWAS 268
 QY 370 SCADLAVECAFRRESGV-IG-HDED 392
 Db 269 KFGAVAVELLQEGKGLCVGIHNE 293

RESULT 8
 US-08-416-870C-8
 ; Sequence 8, Application US/08416870C
 ; Patent No. 5824862

; GENERAL INFORMATION:
 ; APPLICANT: HIYOSHI, TORU
 ; APPLICANT: KASHIOKA, KEISUKE
 ; APPLICANT: TYSON, ROBERT HOW
 ; APPLICANT: PAGE, ANTHONY MILES JOHN
 ; TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
 ; TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTO
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
 ; STREET: PO BOX 747
 ; CITY: FALL CHURCH
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22040-0747
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/416,870C
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURPHY JR, GERALD M
 ; REGISTRATION NUMBER: 28,977
 ; REFERENCE/DOCKET NUMBER: 760-195P(PCT)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 205-8000
 ; TELEFAX: (703) 205-8050
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 522 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-416-870C-8

Query Match 9.3%, Score 211.5, DB 2, Length 522.

Best Local Similarity 23.7%, Pred. No. 3,6e-12;
 Matches 98; Conservative 69; Mismatches 168; Indels 79; Gaps 15;
 QY 34 KVALTAGGLAPCLNSAISGLIERYTEIDPSIEIC-----YRGGY-KGLLGDSYPTVA 87
 Db 166 KVALITCGGLCPGLNDVIRQIV--FTLETYGVKNIIVGIFPGYRPFREKGL---KEMPLSR 220
 QY 88 EVRKAGVLRQFGSSVIGNSRYKLTINVKDCVKGGLVKGGEDEPOKVAADQLVQGDVILHT 147
 Db 221 DVVEN-----INLSGSGFLG-----VSRGAKTISE-----IVDSIQARRIDMEFEV 260
 QY 148 TGGDDNTTAADLAFLANNVGLTVIGPKVNDVPPFKISLGANTRAEQARFPMV 207
 Db 261 TGGNSHGAGANAIIHEECRKLKAVVAVPKTIDILFMDKTFGPDIVESAQRILNSA 320
 QY 208 VANNANPRLIVHEVGRNCGMLTAATAOEYRKLDRAMELPELGTRESEYHAAVFP 267
 Db 321 YIARSAYHIGLVLMGSSGFIA-----MHASLSGQIDVCLIP 361
 QY 268 EWAIDLEAAKRLREVMDKVD-----CVNIFVSEGAIVEAIVAEWQAKGGEVPRDARFHK 323
 Db 362 EVSFTLDGERGVLRHLEHLNTRKFCV-VCAVEGAGQDL-----QSNATDASGVY 413
 QY 324 IDAVNPGKMFGEQFAQMI-----GAETLYQSGGYFAPASAVNDKRLIKSCADL 374
 Db 414 LSD-----FGVHMQKIKKHFKDQIGPADLKYIDPT-YMVAAACRANSDALICTVLQGN 466
 QY 375 AVECAFRRESGVITGDEDNGVLAIRPEPRIKGKRPNIDTFNSMLSEIGOP 428
 Db 467 AVHGAFAGPSGITSGVCNTHVYLRPT-EVITTPHVNPNNSMWRCLTSTQOP 519

RESULT 9
 US-08-280-690-2

; Sequence 2, Application US/08280690
 ; Patent No. 5583011
 ; GENERAL INFORMATION:
 ; APPLICANT: Mansour, Tag B
 ; TITLE OF INVENTION: Compositions, Treatments, and
 ; TITLE OF INVENTION: Diagnostics for Schistosomiasis and Related Diseases
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Goddard
 ; STREET: 5 Palo Alto
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306-2155
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/280,690
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Nealey, Richard L
 ; REGISTRATION NUMBER: 30,092
 ; REFERENCE/DOCKET NUMBER: STAN-141/00US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-843-5070
 ; TELEFAX: 415-857-0663
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 781 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-280-690-2

US-09-198-452A-458
 ; Sequence 458, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffiths, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 845
 ; SEQ ID NO 458
 ; LENGTH: 845
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 ; US-09-198-452A-458

Query Match 5.0%; Score 113.5; DB 4; Length 845;
 Best Local Similarity 21.5%; Pred. No. 0.033;
 Matches 117; Conservative 73; Mismatches 170; Indels 185; Gaps 30;

QY 30 NDKKVAITLFGG---LAPCLNSAIGSLIERYTEIDPSIBIIICRGYKGLLDGSDYPT 86
 DB 179 DKNEKLSALTAIYGYDLTETMRKSLDPVIGSSSEVEKIIILCRKRNPNVILGE----- 233
 QY 87 AEVRKA---GYLORFGSVIGNSRYKLTNVKDCVR-----GLVKEGEDPQ 130
 DB 234 AGVKATPAIVEGLAQ-----KIILNEVPDLARKKELITDLALMTAGTYKRGQFE 283
 QY 131 KVA---DQVKGDS---VDLFTIGDDDTNTAAD---LAFLARN---YGLTVI-- 174
 DB 284 RIVAVMDEVKRGHIIILPDELFTIVGAGAAEADISNLKRALRGITQIGATTID 343
 QY 175 -----GLPXTVD--NDVPIKOST--GAWTAAB 198
 DB 344 YRKHEDKALERRPQKIVVHPSPVDETIELRLKKVYBEHNHNVITTEBALKAATLS 403
 QY 199 Q-----GARYFNVAENNAAPMLIVHEFMGRCMLTATQOER 240
 DB 404 QYVHGRFLPDKALDLDGAGARVNTMQ--PTDLMKEAELENTKLAKEQAIQOBYE 461
 QY 241 K---LIDRAEMLPB-LGLTRESY-----EYHAFVPEMAID-----LEAAK 278
 DB 462 KAGGLDBEKGKLERQSMQKEHKEHQPVDENAVAGVSLGTGIPSAALTAESB 521
 QY 279 REFEVND---KVDCAVIFVSEGAIVEAEMQ-----AKGGEVPRDAFGHIKIDAVNP 329
 DB 522 KILKLEDTLRRKY-----IGQNDATVSTICRAIRRSRTGIDPNRPTGSF--LFLGPTGV 573
 QY 330 GK-WPEBOPF-OMIGAKXTLYQ--KSGYFARASAVVDKRLKSGADLAVBGAFFRESG 365
 DB 574 GSKLLAQQLIIEFGGSDALIQVMSBYMEKFPATQK-----MGSPFG 616
 QY 386 VIGHEDDNGNVLAIE-----FPIKGGKPFNIDTWPNSMLSEIGQPK-----GSK 432
 DB 617 YVGH-BEGGHLTQVRRRRCYCVLFPEIEKAP-----DINDMLQILGGRITDSFGK 670
 QY 433 VEVSH 437
 DB 671 VDFRH 675

RESULT 13
 US-09-541-782-4
 ; Sequence 4, Application US/09541782
 ; Patent No. 6284480
 ; GENERAL INFORMATION:
 ; APPLICANT: Nislow, Corey
 ; APPLICANT: Sakowicz, Roman
 ; APPLICANT: Beraud, Christophe
 ; TITLE OF INVENTION: Antifungal Assay
 ; FILE REFERENCE: 1015

CURRENT APPLICATION NUMBER: US/09/541,782
 ; CURRENT FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 1038
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 ; US-09-541-782-4

Query Match 4.4%; Score 99.5; DB 3; Length 1038;
 Best Local Similarity 20.7%; Pred. No. 1.1;
 Matches 85; Conservative 65; Mismatches 160; Indels 101; Gaps 18;

QY 47 LNSAIGSLIERYTEIDPSIBIIICRGYKGLLDGSDYPTAEVRKAGVLFQSGSVIGN 106
 DB 685 LNTMOGESILQETINQPNIDMI-----KNEVLITRMQKAEIM----- 724
 QY 107 SRVRLTNVDCVR-----GLVKEGEDPQYAADQVLDGVDILHTIGDDTNTAA 157
 DB 725 -----YDCVYKXILNESPKFFNVVTEKIDIRVDQFKFYNNIAENTSDISENNMRQ 777
 QY 158 ADLAAFLANNNGLVIGPKTVNDVFPKOSLGAWTAABGARYENNVAVENNANP 217
 DB 778 YLKNHFPKNNHQL-----LNRHVDSTYENTER-----RTNFVENFKVLDHLDENK 827
 QY 218 LIVHEVMGRCMLTAAAOEYRKLID-----RAEMLPELGLTRESYEYHAFVPEMAID 272
 DB 828 LHMN-----LTTASAVIDQEMDLFEPKRVKWEKNSFDLINDCSNNNEFYNSMAAT 879
 QY 273 LEAEKRLREYNDKPCVNIPIVSEGAIVEAEMQAGQ--EVRPDAPFHILDLAVNP 331
 DB 880 IS-----QIKSTVDTSSSNESISV-----MNGQVESINALSLLK---INTK 920
 QY 332 WPEQFAQWIGAETL---VQSGYFARASAVNDM-----FLIKSGADLAVBGAFFRE 383
 DB 921 -FNDQFBDLINHNNLKNINISITSHITNVODIYNTIENIMKNYGN-----KG 971
 QY 384 SCVTHEDDNGNVLAIEFPIKGGKPFNIDTWPNSMLSEIGQKQKVE 434
 DB 972 NAT--KDEMTENILK--EIPNLISKMPPLNSINSVQSVL-SPKDAIE 1017

RESULT 14
 US-09-723-820-4
 ; Sequence 4, Application US/09723820
 ; Patent No. 6468760
 ; GENERAL INFORMATION:
 ; APPLICANT: Nislow, Corey
 ; APPLICANT: Sakowicz, Roman
 ; APPLICANT: Beraud, Christophe
 ; TITLE OF INVENTION: Antifungal Assay
 ; FILE REFERENCE: 1015
 ; CURRENT APPLICATION NUMBER: US/09/723,820
 ; CURRENT FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 09/541,782
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 1038
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 ; US-09-723-820-4

Query Match 4.4%; Score 99.5; DB 4; Length 1038;
 Best Local Similarity 20.7%; Pred. No. 1.1;
 Matches 85; Conservative 65; Mismatches 160; Indels 101; Gaps 18;

QY 47 LNSAIGSLIERYTEIDPSIBIIICRGYKGLLDGSDYPTAEVRKAGVLFQSGSVIGN 106
 DB 685 LNTMOGESILQETINQPNIDMI-----KNEVLITRMQKAEIM----- 724

```

QY 107 SRVRLTNVDCVKR-----GLVKEGEDPQKVAADQLVKDVILHTIGDDDTNAA 157
| | | | |
DB 725 -----YKDCVKKILNESPKEFNVIIEKIDIRVDFPKFNIAENLSDISENNMKQ 777
| | | | |
QY 158 ADLAAFLARNYGLTVLPTVNDVFPFKOSLGAWTAAGAGYFNNVVAENANPRM 217
| | | | |
DB 778 YLKNHFFPNKHQEL-----LNRHVDSTYENIEK-----RTNEFVENFKVLNDHLENKK 827
| | | | |
QY 218 LIVHEWGRNGCWLTAATAOEYKLLD-----RAEMLPGLTRESYEVAHVPYENAI 272
| | | | |
DB 828 LHMN-----LFTATSAVIDQMDLFEPKRYWENSPLLINDCSMNNEFYNSMAAT 879
| | | | |
QY 273 LEAEAKRREVMKDCVNIFVSEAGYEAIAENQAGQ-EVRPDAFGHKLDAVNPCK 331
| | | | |
DB 880 LS-----QIKSTVDTSNSNNEISY-----MRQVESEENALSLK-----NNTX 920
| | | | |
QY 332 WEGQFAQWIAEKL-----VOKSGYFARASAVNDM-----RLIKSCADLAVECAFRE 383
| | | | |
DB 921 -FNDQFQILNKNLKNKINISITSHITNDVINTENTENIMKNYGN-----KE 971
| | | | |
QY 384 SGVIGHDEDNQVLAIEPPRIKSGKPFNIDTWENSLSEIGQKSGKVE 434
| | | | |
DB 972 NAT--KDEWIENILK--EIPMLSKMPLRLSNINSVOSVI--SPKKHAIR 1017
| | | | |

```

RESULT 15

```

US-09-328-352-6730
; Sequence 6730, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328, 352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6730
; LENGTH: 863
; TYPE: PR
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6730

```

Query Match 4.2%; Score 96; DB 4; Length 863;
 Best Local Similarity 20.9%; Pred. No. 1.8; Mismatches 157; Indels 168; Gaps 26;
 Matches 104; Conservative 69;

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QY 27 TLANKPKVAIL-TNGIAPCLNSAI-GSLERTYETIDPSITRIICRYGGYGLLGDSYP 84
| | | | |
DB 41 TLLEPNSISLQAGARLPKQLKQALDAPFIANPTGDVNLNPEAVPALNADRVA 100
| | | | |
QY 85 V-----TAVRKKAGVLQRFQSVIGNSRVKLTNVDKCVKRLVKEGEP 129
| | | | |
DB 101 QKAGBFLSTBWVLLGLAETGETKNIL-----SANGVTPDSLRYIENI-RGSDKMSNN 154
| | | | |
QY 130 QKVAADQLVKQGVILH-----TIQGDPTNTAADLAAFLARN-----YGLT 172
| | | | |
DB 155 HEDQDSINKYITIDTERALSGKLDPIVGRDDEIRITQVLSRTKNNPVLIGEPGVGT 214
| | | | |
QY 173 VI--GLPKTVNDVFP-----IKOSIGAMTAAGAGY-----FMNVVAENN 212
| | | | |
DB 215 AIVSGIAQIVNGEYBGLKRVKVLSDLSLA---GAKYRGFEFERLKAVALKDLAAGH 271
| | | | |
QY 213 ANPRMLI--VHEWGRNGC-----WLTAAATAOEYKLLDRAEWL- 249
| | | | |
DB 272 GEIILFIDELHTLVGAGKDDGAMGAMWELKPALANGELRCVGAFTLDEYRIEKDALE 331
| | | | |
QY 250 -----PELGLT-----RESYEVH-----AVF-----VPEMA 270
| | | | |
DB 332 RRFQKVLVDEPSEVEDTIALRLGIEKKYATHGVOILDSALITAAANMSHRYITTDQLDPKA 391
| | | | |
QY 271 IDL--EAEAKRLR-----EVMDKVD-----CVNIFVSEAGYEAIAENQAGQOE 313
| | | | |

```

```

DB 392 IDLIDEAASRIKWEIDSKPEALDKLDRLLIQLMQLEAVKQEDAGSKAEVTHLEKQIAE 451
| | | | |
QY 314 VPDPAFGHKLDAVNPCKMFGSQFAQWIAEKLTVOKSGYFARASAVNDMLIKSCA- 372
| | | | |
DB 452 VKE-----YNDLEEV-----KAEKTLVSGT-----KQAVYELDKARIAFEKAQ 491
| | | | |
QY 373 ---DLAVECAFRESGVI 387
| | | | |
DB 492 REGDLAE--AARLOYGVI 507
| | | | |

```

Search completed: January 29, 2004, 14:39:01
 Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 14:32:17 ; Search time 21 Seconds
(without alignments)
2001.224 Million cell updates/sec

Title: US-09-941-947a-2

Perfect score: 2284

Sequence: 1 DVTMPHYLTDIRCHWF.....FNSLSEIGPKGKVRVSH 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1314	57.5	408	2	A41169
2	1298.5	56.6	479	2	AC2836
3	1298.5	56.6	514	2	P97613
4	311	13.6	342	2	T35500
5	270	11.8	448	1	F70190
6	263.5	11.5	436	1	S49458
7	257.5	11.3	500	2	T06011
8	253	11.1	319	2	C72406
9	251	11.0	473	2	T13433
10	246.5	10.8	987	1	J00016
11	245.5	10.7	992	2	S32902
12	243	10.6	462	2	T10691
13	241.5	10.6	437	2	S54978
14	240.5	10.5	320	2	AH0942
15	238.5	10.4	320	1	KIECPA
16	238.5	10.4	320	2	A86081
17	238.5	10.4	320	2	A88234
18	238.5	10.3	327	2	AP0010
19	233.5	10.2	322	2	S39248
20	233	10.2	319	2	S35928
21	232	10.2	461	1	A71366
22	226	9.9	322	1	UQ1028
23	224.5	9.8	334	2	A75495
24	223.5	9.8	319	2	D84045
25	223.5	9.8	331	2	G82045
26	223	9.8	343	2	E70856
27	222	9.7	340	1	UN0614
28	221	9.7	335	2	D97971
29	220	9.6	573	2	C71312

30	220	9.6	780	1	KIRBF	6-phosphofructokin
31	216.5	9.5	319	2	F96963	6-phosphofructokin
32	215	9.4	335	2	F95103	6-phosphofructokin
33	213.5	9.3	321	2	C70447	phosphofructokinase
34	211.5	9.3	348	2	T45407	phosphofructokinase
35	210.5	9.2	320	2	R84965	6-phosphofructokin
36	210.5	9.2	343	2	G87121	6-phosphofructokin
37	210.5	9.2	544	2	S52081	6-phosphofructokin
38	210	9.2	780	1	KIHUFM	diphosphate-fructo
39	210	9.2	789	1	KIHUFM	6-phosphofructokin
40	209	9.2	319	1	KIBSFE	6-phosphofructokin
41	209	9.2	323	1	G64223	6-phosphofructokin
42	207.5	9.1	791	2	A53205	6-phosphofructokin
43	207	9.1	959	1	J00017	6-phosphofructokin
44	204.5	9.0	784	2	UC2055	6-phosphofructokin
45	204	8.9	463	2	B84613	hypothetical prote

ALIGNMENTS

RESULT 1
A41169
diphosphate-fructose-6-phosphate 1-phosphotransferase (BC 2.7.1.90) - Propionibacterium
N:Alternate names: 6-phosphofructokinase (pyrophosphate)
C:Species: Propionibacterium freudenreichii
C>Date: 17-Jul-1992 #sequence_revision 14-Apr-2003 #text_change 14-Apr-2003
C/Accession: A41169
E/Ladror, U.S.; Gollapudi, L.; Tripathi, R.L.; Latehaw, S.P.; Kemp, R.G.
J. Biol. Chem. 266, 16550-16555, 1991
A:Title: Cloning, sequencing, and expression of pyrophosphate-dependent phosphofructokin
A:Reference number: A41169; MUID:91358443; PMID:1653240
A:Accession: A41169
A:Molecule type: DNA
A:Residues: 1-404 <LAD>
A:Cross-references: GB:M67447; NID:g150930; PIDN:AA25675.1; PID:g150931
C:Comment: This is an example of a nonallosteric, pyrophosphate-dependent phosphofructoki
F:Keywords: phosphotransferase
F:5-322/Domain: 6-phosphofructokinase 1 homology <6PFI>

Query Match	57.5%	Score 1314;	DB 2;	Length 408;
Best Local Similarity	62.6%	Pred. No. 4.2e-66;		
Matches 248;	Conservative 60;	Mismatches 88;	Indels 0;	Gaps 0;
QY	33	KRYAIIITAGGLAPCINSATISLIERTEIDPSIITCYRGYGLIGDSYPTAVYKX	92	
DB	7	KRYAIIITAGGLAPCINSATISLIERTEIDPSIITCYRGYGLIGDSYPTAVYKX	66	
QY	93	AGYLQRFQSGSVIGNSRYKLTNVVDQVYKGLVKEGDDPQRYAADQLVKGVDIHTIGDD	152	
DB	67	YDRLFQFGSGPIGNSRYKLTNVVDQVYKGLVKEGDDPQRYAADQLVKGVDIHTIGDD	126	
QY	153	TNTRAADIAAFIARNNVGLTVIGLPTKVDNDVPIRQSGIAGMTAARGANVFNVAENN	212	
DB	127	TNTRAADIAAFIARNNVGLTVIGLPTKVDNDVPIRQSGIAGMTAARGANVFNVAENN	186	
QY	213	ANPRMLIVHVMGRNCGWLTAAQYRKELDRAEWLPIKGLTRBSYBVAIVFPEMAID	272	
DB	187	AAPRELIHHRMGRNCGWLTAAQYRKELDRAEWLPIKGLTRBSYBVAIVFPEMAID	246	
QY	273	LEAEARLEBVNDKDCVNTIFVEEGAGVATVAKAKQGVPRDPAFGHKLDAUNRGK	332	
DB	247	LDAAERLEBVNDKDCVNTIFVEEGAGVATVAKAKQGVPRDPAFGHKLDAUNRGK	306	
QY	333	FGQPAQMIKAETLVQKSGYFAPASASVNDWRLLKSCADLAVECAFRESGVIGHED	392	
DB	307	FAQPAERIGAGTIVQKSGYFAPASASVNDWRLLKSCADLAVECAFRESGVIGHED	366	
QY	393	NGVTLAIEPRPKGKGPNIIDTWKNSMLSEIGOP	428	
DB	367	AGKSLVIDPKIAGHKKPDITLDWYTLARIGOP	402	

RESULT 2
AC2836
Hypothetical protein pfp [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C/Species: *Agrobacterium tumefaciens*
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 14-Apr-2003
C/Accession: AC2836
R/Mood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Mo, L.
erage, G.; Gillet, W.; Grant, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AC2836
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-479 <KUR>
A/Cross-references: GB:AE006868; PIDN:AL43105.1; PID:g17740576; GSPDB:GN00186
A/Experimental source: Strain C58 (Dupont)
C/Genetics:
A/Map position: circular chromosome
C/Superfamily: pyrophosphate dependent phosphofructokinase; 6-phosphofructokinase 1 hom

Query Match 56.6%; Score 1292.5; DB 2; Length 479;
Best Local Similarity 57.9%; Pred. No. 1.8e-84;
Matches 246; Conservative 71; Mismatches 101; Indels 7; Gaps 2;

QY 8 HLTADL-----RCHMFPLNPNFYTLNKKKVAIITAGLAPCLNSAGISLIEREYIDP 63
Db HLTAAVASICQCTLMVYAK--RRAMAKQKVAIITAGLAPCLNSAGISLIEREYIDP 110
QY 64 SIEIICRGYKGLLDGDSYPTAEVRKKAGVLOFGSGVIGNSRVKLTNNVDCVGRGLV 123
Db EIDIIAVRSYGCVGLLGERIEITKMRKALHHRYGSGPIGNSRVKLTNNVDCVGRGLV 170
QY 124 KEGEDPQKVAADQVYKQGVDIITHTGGDPTNTAAADLAAPLARNNGYLVIGLPTVND 183
Db KEGEDPQKVAADQVYKQGVDIITHTGGDPTNTAAADLAAPLARNNGYLVIGLPTVND 230
QY 171 KEGEDPQKVAADQVYKQGVDIITHTGGDPTNTAAADLAAPLARNNGYLVIGLPTVND 230
Db 171 KEGEDPQKVAADQVYKQGVDIITHTGGDPTNTAAADLAAPLARNNGYLVIGLPTVND 230
QY 184 VEPITKOSLGAMTAABEGARFMNVVAENANPRLIYHEVWGRNGCMITATAOEYRKL 243
Db VEPITKOSLGAMTAABEGARFMNVVAENANPRLIYHEVWGRNGCMITATAOEYRKL 290
QY 231 VEPITKOSLGAMTAABEGARFMNVVAENANPRLIYHEVWGRNGCMITATAOEYRKL 290
Db VEPITKOSLGAMTAABEGARFMNVVAENANPRLIYHEVWGRNGCMITATAOEYRKL 303
QY 244 DRAEWLPGLTRESYEVHVAIVPEMAIDLEAKRLREVMKVCVNCNIFVSEAGVEAI 303
Db DRAEWLPGLTRESYEVHVAIVPEMAIDLEAKRLREVMKVCVNCNIFVSEAGVEAI 350
QY 291 KANDYVBGLMMNTQKNIIDGILPEMAFDIAERLKEVMDKGYTLTFVSEAGVDAI 350
Db KANDYVBGLMMNTQKNIIDGILPEMAFDIAERLKEVMDKGYTLTFVSEAGVDAI 363
QY 304 VAEWQAKQGVPRDAFGHIKLDVAVNPKMFGEGQPAQMITGAETLVKSGYFARASASND 363
Db VAEWQAKQGVPRDAFGHIKLDVAVNPKMFGEGQPAQMITGAETLVKSGYFARASASND 410
QY 351 VAEWQAKQGVPRDAFGHIKLDVAVNPKMFGEGQPAQMITGAETLVKSGYFARASASND 410
Db VAEWQAKQGVPRDAFGHIKLDVAVNPKMFGEGQPAQMITGAETLVKSGYFARASASND 423
QY 364 DMLILKSCADLAVECAFRESGVIGHDEONGVLAIEPPIKSGRPNTDITDWFNMLS 423
Db DMLILKSCADLAVECAFRESGVIGHDEONGVLAIEPPIKSGRPNTDITDWFNMLS 470
QY 411 DMLILKSCADLAVECAFRESGVIGHDEONGVLAIEPPIKSGRPNTDITDWFNMLS 470
Db DMLILKSCADLAVECAFRESGVIGHDEONGVLAIEPPIKSGRPNTDITDWFNMLS 470
QY 424 EIGQP 428
Db 424 EIGQP 475

RESULT 3
P97613
pfp-1-phosphofructokinase (AF246209) [imported] - *Agrobacterium tumefaciens* (strain C58, C/Species: *Agrobacterium tumefaciens*
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 14-Apr-2003
C/Accession: P97613
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Mollan, C.; Allinger, M.; Doughty, D.; Scott, C.; Dappas, C.; Markez, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: P97613
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-514 <KUR>
A/Cross-references: GB:AE007669; PIDN:AAK7863.1; PID:g15157249; GSPDB:GN00186
C/Genetics:
A/Map position: circular chromosome
A/Map position: circular chromosome

Query Match 56.6%; Score 1292.5; DB 2; Length 514;
Best Local Similarity 57.9%; Pred. No. 2e-84;
Matches 246; Conservative 71; Mismatches 101; Indels 7; Gaps 2;

QY 8 HLTADL-----RCHMFPLNPNFYTLNKKKVAIITAGLAPCLNSAGISLIEREYIDP 63
Db HLTAAVASICQCTLMVYAK--RRAMAKQKVAIITAGLAPCLNSAGISLIEREYIDP 145
QY 64 SIEIICRGYKGLLDGDSYPTAEVRKKAGVLOFGSGVIGNSRVKLTNNVDCVGRGLV 123
Db EIDIIAVRSYGCVGLLGERIEITKMRKALHHRYGSGPIGNSRVKLTNNVDCVGRGLV 205
QY 124 KEGEDPQKVAADQVYKQGVDIITHTGGDPTNTAAADLAAPLARNNGYLVIGLPTVND 183
Db KEGEDPQKVAADQVYKQGVDIITHTGGDPTNTAAADLAAPLARNNGYLVIGLPTVND 265
QY 184 VEPITKOSLGAMTAABEGARFMNVVAENANPRLIYHEVWGRNGCMITATAOEYRKL 243
Db VEPITKOSLGAMTAABEGARFMNVVAENANPRLIYHEVWGRNGCMITATAOEYRKL 325
QY 244 DRAEWLPGLTRESYEVHVAIVPEMAIDLEAKRLREVMKVCVNCNIFVSEAGVEAI 303
Db DRAEWLPGLTRESYEVHVAIVPEMAIDLEAKRLREVMKVCVNCNIFVSEAGVEAI 385
QY 304 VAEWQAKQGVPRDAFGHIKLDVAVNPKMFGEGQPAQMITGAETLVKSGYFARASASND 363
Db VAEWQAKQGVPRDAFGHIKLDVAVNPKMFGEGQPAQMITGAETLVKSGYFARASASND 445
QY 386 VAEWQAKQGVPRDAFGHIKLDVAVNPKMFGEGQPAQMITGAETLVKSGYFARASASND 445
Db VAEWQAKQGVPRDAFGHIKLDVAVNPKMFGEGQPAQMITGAETLVKSGYFARASASND 505
QY 424 EIGQP 428
Db 424 EIGQP 510

RESULT 4
T35500
6-phosphofructokinase (BC 2.7.1.11) - *Streptomyces coelicolor*
C/Species: *Streptomyces coelicolor*
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 12-May-2003
C/Accession: T35500; T42063
R/Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A/Reference number: Z21580
A/Accession: T35500
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-342 <SEB>
A/Cross-references: EMBL:AL09661; PIDN:CAB51967.1; GSPDB:GN00070; SCODEB:SCGE10.13c
A/Experimental source: strain A3(2)
R/Alves, A.M.; Ruvierink, G.J.; Bibb, M.J.; Dijkhuizen, L.
Appl. Environ. Microbiol. 63, 956-961, 1997
A/Title: Identification of ATP-dependent phosphofructokinase as a regulatory step in the
A/Reference number: Z22050; MUID:9708211; PMID:9055413
A/Accession: T42063
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-342 <ALV>
A/Cross-references: EMBL:U51728; NID:g1931572; PIDN:AAK45135.1; PID:g1931573
C/Genetics:
A/Map position: circular chromosome
C/Superfamily: 6-phosphofructokinase, bacterial type; 6-phosphofructokinase 1 homology

C:Keywords: ATP; glycolysis; phosphotransferase

Query Match 13.6%; Score 311; DB 2; Length 342;

Best Local Similarity 27.4%; Pred. No. 1e-14;

Matches 105; Conservative 63; Mismatches 137; Indels 78; Gaps 17;

34 KVALITAGGLAPCLNSAIGSLERYTEIDPSEIICRYGGYKGLLGDSPYTAAYRKA 93

2 KQVGLVGGGDCPEGLMNVIRAVKGVQ-EKGYDFGFRGMRPLSGDVPPL-DIPAR 58

94 GVLQRFSGSVIGNSRYKLTNVKDCVKRGLVKGSDPQKVAADQVKGVDILHTTGGDT 153

59 GLIFR-GGVYIGSSRNPPLKORDIR-----IKDIALGVEALITTGSDT 105

154 NFAAADLAAFLAANNGLTVIGLPTVNDVFPKQSLGAMTAAGGARYFNVAENNA 213

106 LGVATLA-----DEGVPCVGPVKTIDLSATDTPGPDTRVAGTATADILHTTAS 160

214 NPMRLIVHEVWGRNCGMLTAATAQERYKLLDRAEWLPELGLTRSEYVHAVPPEMAIDL 273

161 HEMLVV-EVWGRHAGMIALHS-----GLAGGA---NVILIPGQPDV 199

274 EA-----EAKRLRWDKDCVNI FVSEGAQVEAIVAEQAKGQVPR---DAFGHIKD 325

200 EGVCSWTSRFRASVAPL-----VVVAEGA-----MRDDDMVLKDSLDLSYGHVRLS 247

326 AVNPGKMFGEQFQMIKAE-KTLVQSGYFAPASASNDPMRLIKSCADLAVECAFRRS 384

248 GV--GEMLAKQIEKRTGNEARTV--LGVVQKGTSPADRLATRFGLHAYDCV----- 298

385 GYIGHEDENGNV--LRAIEFPRI 405

299 ---HDDGFGKVAIFGTIVRV 317

RESULT 5

F70190

probable diphosphate-fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) - Lyme dise

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 14-Apr-2003

C:Accession: F70190

A:Author: C.M.; Castens, S.; Huang, M.M.; Sutmon, G.G.; Clayton, R.; Lachygra, R.; White

A:Ref: Peterson, J.; Kervage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

A:Ref: Nature 390, 580-586, 1997

214 NPMRLIVHEVWGRNCGMLTAATAQERYKLLDRAEWLPELGLTRSEYVHAVPPEMAIDL 273

244 AVNPGKMFGEQFQMIKAE-KTLVQSGYFAPASASNDPMRLIKSCADLAVECAFRRS 384

274 EAE-----AKEL-REVMQKDCVNI FVSEGAQVEAIVAEQAKGQVPR---DAFGHI 322

265 EGNPGFVHLERRLKESLSBEIPHAVALIABAG-----QYFDFPKKODSGTL 336

323 KLDVNPCKMFGEQFQMIKAEK--TLVQ-KSGYFAPASASNDPMRLIKSCADLAVECF 378

337 LYEDI--GLYIKDKITFEYKAKNIQTLKYIDPSYIIRSSPAMADSDLYCARLSNAVA 394

379 AFRRSGYIGHEDENGNV--LRAIEFPRIKGPENIDTDMNSMSEIQP 428

395 KAGKTNLILSMSTKFEVHTPIKNAVTDNRK-VNPNQSGFMVDVASTGP 443

RESULT 6

S49458

diphosphate-fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) (validated) - Entamo

C:Species: Entamoeba histolytica

C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 14-Apr-2003

C:Accession: S49458; S68243; S52082

A:Author: R. Bruchhaus, I.

A:Ref: submitted to the EMBL Data Library, October 1994

A:Reference number: S49458

A:Accession: S49458

A:Molecule type: mRNA

A:Residues: 1-436

A:Cross-references: EMBL:X82173; NID:G558573; PIDN:CAAS7659.1; PID:G558574

R.Bruchhaus, I.; Jacobs, T.; Denart, M.; Tannich, B.

Biochem. J. 316, 57-63, 1996

A:Title: Pyrophosphate-dependent phosphofructokinase of Entamoeba histolytica: molecular

A:Reference number: S68243; MUID:96235172; PMID:8645233

A:Accession: S68243

A:Molecule type: mRNA

A:Residues: 1-429, 'T', 'A', '31-436

A:Cross-references: EMBL:X82173; NID:G558573

A:Note: the authors present evidence of the enzymes activity

A:Note: the authors present evidence of the enzymes activity

A:Note: the authors present evidence of the enzymes activity

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A:Note: the authors present evidence of the enzymes activity

A:Note: the authors present evidence of the enzymes activity

Db 242 KSANNGIGIVLWGRDAGFTAL-----YASLANG-----DANVLIPEDID 282

Qy 272 DL-----SAAKRLAEVNDKYDCVNI FVSEAGAVEAIVAEKQGEVPRAPGHI-KLDA 326

Db 283 PIQIGCFVKR---INSGHV-IVABGA-----LQNKRPDLIDIGTDSNIIHMS 333

Qy 327 VNRKMGGEQPAQMTGAEKLVQ--KSGYFARASASVNDKRLIKSCADLAVCAFRRES 384

Db 334 INVLRSITLYKSGIGIEHTIKFVDPSTYKRSAPCAADHPCKMCLANAAVAVAGKX 393

Qy 385 G-VIGHEDGNVYRAIEFPR---IKGKPFNIDTW-FNSMSEIGQPK 429

Db 394 GLVICHNN---FVSYPIDRTSYIK-----RVNIDGPLYTMSAIEKX 436

RESULT 7

T06011
probable diphosphate-fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) T25K17.80
N:Alternate names: protein T25K17.80
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 14-Apr-2003
C:Accession: T06011
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15382
A:Accession: T06011
A:Molecule type: DNA
A:Residues: 1-500 <BEV>
A:Cross-references: EMBL:AL049171; GSPDB:GN00062; ATSP:T25K17.80
A:Experimental source: cultivar Columbia; BAC clone T25K17
C:Genetics:
A:Gene: ATSP:T25K17.80
A:Map position: 4
A:introns: 46/2; 59/3; 80/3; 141/3; 194/3; 212/3; 235/3; 279/1; 367/3; 383/1; 434/3
C:Superfamily: pyrophosphate dependent phosphofructokinase; 6-phosphofructokinase 1 homoc
C:Keywords: phosphotransferase

Query Match 11.3%; Score 257.5; DB 2; Length 500;
Best local similarity 25.6%; Pred. No. 1,1e-10;
Matches 109; Conservative 59; Mismatches 167; Indels 91; Gaps 16;

Qy 37 ILTAGLAPCLNSAIGSL-----IERYTEIDPSIEIIC-----YRGYKGL 78

Db 92 IIVCGGCLPGLNTVIRIVISLSYMGVKKILGIVS---FCDNMLFTKTNNGYRGY 148

Qy 79 LGSYPTAAEVRKKAAGLQRRGSGVIGNSRVKLTNVDCYKGLVREGDPKVAADQV 138

Db 149 AKIVTSIDSKV---VNDIHRGGTILGTSR-----GHDITKI-VDSIQ 188

Qy 139 KDGVDILHTIGDDTNTAAADLAFLARNVGLTVIGLPTVDNDVFPFKOSIGAWTAAE 198

Db 189 DRGIVGVYIIIGDGTGAGAVIFEEIRRGKLVAVIGIDPIKTIQNDIPVIDKSGFDVAE 248

Qy 199 QGARFVNVAENRANRMLTYHEWGRNGMLTAATAGYRKLDBAEMLPELGITRES 258

Db 249 EAORAINAAVESESLENGIGVKKMGKRYSGFLA-----KYATLAS 289

Qy 259 YEYAAVFPMAIDLEAA-----KRLREVNDKYDCVNI FVSEAGAVEAIVAEKQAG 311

Db 290 RDVDCCLIPSPFLYEBEGGLFEYIERKLKESGHW---LVIAKGGQIMSKSMESM- 344

Qy 312 QEVPRAFGHILKDAVNVKGFVBEQPAQMTGAETLVQ---KSGYFARASASVNDMEL 367

Db 345 --TLKASGKMLKDV--GLMLOSIRKHFNOKRMVNTKYIDPTVMIRAVPSNADNY 400

Qy 368 IKSCADLAVCAFRRESGVIGHEDGNV---LRAIEFPKIGKGFNIDTW-FNSMSE 422

Db 401 CTLLAGAAHGAAGYGYI-----SGLVNGRQTYIPFYITKQKHVVITDMAR-LL 454

Qy 423 SETGQ 428

Db 455 SSTQOP 460

RESULT 8

C72406
6-phosphofructokinase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 12-May-2003
C:Accession: C72406
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sex
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72406
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <ARN>
A:Cross-references: GB:AE001705; GB:AE000512; NID:g4980694; PIDN:AA035301.1; PID:g498071
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0209
C:Superfamily: 6-phosphofructokinase, bacterial type; 6-phosphofructokinase 1 homology
F:4-279/Domain: 6-phosphofructokinase 1 homology <6FF>

Query Match 11.1%; Score 253; DB 2; Length 319;
Best local similarity 26.6%; Pred. No. 1.3e-10;
Matches 95; Conservative 60; Mismatches 126; Indels 76; Gaps 14;

Qy 33 KKVAILTAGLAPCLNSAIGSLIERYTEIDPSIEIICYRGYKGLLDSPYPTAEVRK 92

Db 2 KKIIVTSGDAPGNAAVAVV-RY-GVRCGLVYIGVRGSGIIDGPF--VKLEYKDV 57

Qy 93 AGVLQRFQSGVIGNSRVKLTNVCKVKGGLVKEGDPKVAADQVLYKGVDLHTIGED 152

Db 58 AKITK-GGTITRTCEPFT-----REGSLAKQCKKKGISBLVVIIGEG 104

Qy 153 TMTAADIAPLARNNGVTVIGLPTVDNDVFPFKOSIGAWTAAEGARFVNVAENN 212

Db 105 SLT-----GAILLYEHNKIPVIGIPATIDNDIGLDMCIGVDTCLNTWDAVQKLDTPAS 159

Qy 213 ANPKVLYHEWGRNGMLTAATAGYRKLDBAEMLPELGITRESYEVHAFVPEMAID 272

Db 160 SHERAFIV-EWGRSGYIALMAG---LVGAE-----ALIVEIIPVD 198

Qy 273 LEAEKRLREV--MDKDCVNI FVSEAGAVEAIVAEKQGEVPRDAFGHIKLDVAVNG 330

Db 199 YSQLDRILIEERRKINSI-IIVAEGLASAVTAR-----HLE----- 236

Qy 331 KWFGEQPAQMTGAETLVOKSGYFARASASVNDMELIKSCADLAVCAFRRESGYI 387

Db 237 -----YRIGYE-TRITIIHVGQSGPTAFDRRLASMGVZAVADLLDGEVDVM 284

RESULT 9

T13433
pyrophosphate-dependent phosphofructo-1-kinase homolog T17A13.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 14-Apr-2003
C:Accession: T13433
R:Bevan, M.; Leonard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro
submitted to the Protein Sequence Database, July 1999
A:Reference number: Z17683
A:Accession: T13433
A:Molecule type: DNA
A:Residues: 1-473 <BEV>
A:Cross-references: EMBL:AL096692; GSPDB:GN00062; ATSP:T17A13.40
A:Experimental source: cultivar Columbia; BAC clone T17A13
C:Genetics:
A:Gene: ATSP:T17A13.40
A:Map position: 4
A:introns: 35/3; 51/2; 64/3; 85/3; 131/3; 202/3; 225/3; 269/1; 358/3; 373/1; 424/3
C:Superfamily: pyrophosphate dependent phosphofructokinase; 6-phosphofructokinase 1 homoc

F:95-405/Domain: 6-phosphofructokinase 1 homology <6PF>

Query Match 11.0%; Score 251; DB 2; Length 473;

Best Local Similarity 25.2%; Pred. No. 3.1e-10;

Matches 103; Conservative 60; Mismatches 174; Indels 72; Gaps 15;

```

QY 37 ILTGGAGLACGSLERTEIDPSIETICRYGKGLLGDSYPTAVRKKAGVL 96
DB 97 ITCGGICPLNATVHEICGLYMGVKKILIDIGIKFARTNTHDL--KTVNDI 153
QY 97 QRFQGVIGNSRVKLTNVKDCVKGKEDPQKVAADQLVGDYDILHTIGDDPTNVA 156
DB 154 HRSQGTILGTSR-----GSHNTTKI-VDSIQRGINGYIILIGDSQSG 196
QY 157 AADLAFLARNTKGLVIGLPTKVDVDPPIKOSLGAMTAAEGCAEYMMVVAENANR 216
DB 197 AALFEIRKRLKLVAVAGIPKTIIDIPIDISFDPDAVEAQAIAAAVEATSPEN 256
QY 217 MLTVEVMGANGCMLTAAATQAEYKLLDRAEWLPEGLTRESYEVAHVPFEMADLEAR 276
DB 257 GIGLVLMGRYSGFIA-----MHATLASRDVDCCLIPSPFFLEGS 297
QY 277 A-----KREHMDKVDCCNIFVSEGAQVEATVAEQAKQOEVRDAFGHIKLDVAVNP 329
DB 298 GGLFEFIDRLKSKSHNV-----IVIAEGAGQDLSESM--KESTTLKDSGKMLQDI-- 349
QY 330 GKWFQGPQPMIGAEKTLVQK---SGYFPAASASNVDMRLKSCADLAVECAFRESGV 386
DB 350 GLNISRIKIDHRAKKKTLTLKTIIDPTMYTRAAPSNSD---NVCTTLAQSVAH---GV 402
QY 387 I-GHDEDNQVLA---IEFPII-KGCKFPNIDPTMNSLSEIGCP 448
DB 403 MAGYNGFTVGLVNGRHTYIPENRITKOKXVITDGMAR-LLSTINOP 450

```

RESULT 10

J00016 6-phosphofructokinase (EC 2.7.1.11) alpha chain - yeast (*Saccharomyces cerevisiae*)

N.Alternate names: phosphofructokinase 1; phosphohexokinase; protein 194; protein G8593;

C.Species: *Saccharomyces cerevisiae*

C.Date: 31-Mar-1990 #sequence revision 14-Jul-1999 #ext change 12-May-2003

C.Accession: J00016; S38963; S57708; S64566; S64564; S61924

R.Helmsch, U.; Ritzel, R.G.; von Borstel, R.C.; Aguilera, A.; Rodicio, R.; Zimmermann, Gene 78, 309-321, 1989

A.Title: The phosphofructokinase genes of yeast evolved from two duplication events.

A.Reference number: A91608; MUID:89378757; PMID:2528496

A.Accession: J00016

A.Molecule type: DNA

A.Residues: 1-987 <HEI>

A.Cross-references: EMBL:M26943; NID:g172137; PIDN:AAA34859.1; PID:g172138

R.Koperechlaeger, G.; Baer, J.; Stettin, E.

Eur. J. Biochem. 217, 527-533, 1993

A.Title: Limited proteolysis of yeast phosphofructokinase. Sequence locations of cleavage

A.Reference number: S38963; MUID:94039086; PMID:8223596

A.Accession: S38963

A.Molecule type: protein

A.Residues: 1-6790-97;197-205;914-921 <KOP>

R.van der Aart, Q.J.M.; Kleine, K.; Steensma, H.Y.

submitted to the EMBL Data Library, June 1995

A.Description: Sequence analysis of the 43 kb CRM1-YIM9-PRT54-SMII-PHO81-YHB4-PFK1 region

A.Reference number: S57708

A.Accession: S57708

A.Molecule type: DNA

A.Residues: 794-987 <VAN>

A.Cross-references: EMBL:X87941; NID:g886908; PIDN:CAA61193.1; PID:g886937

R.Guerreiro, P.; Barreiro, T.; Azevedo, D.; Rodrigues-Pousada, C.

submitted to the Protein Sequence Database, May 1996

A.Reference number: S64565

A.Accession: S64566

A.Molecule type: DNA

A.Residues: 1-987 <GUA>

A.Cross-references: EMBL:Z73025; NID:g1323434; PIDN:CAA97268.1; PID:g1323435; GSPDB:GN00

A:Experimental source: strain S288C

R:van der Aart, Q.J.M.; Steensma, H.Y.

A:Submitted to the Protein Sequence Database, May 1996

A:Reference number: S64541

A:Accession: S64564

A:Molecule type: DNA

A:Residues: 794-987 <VAN>

A:Cross-references: EMBL:Z73025; GSPDB:GN00007; MIPS:YGR240C

A:Experimental source: strain S288C

R:van der Aart, Q.J.M.; Kleine, K.; Steensma, H.Y.

Yeast 12, 385-390, 1996

A>Title: Sequence analysis of the 43 kb CRM1-YIM9-PRT54-DIR2-SMII-PHO81-YHB4-PFK1 region

A:Reference number: S63896; MUID:96267763; PMID:8701610

A:Accession: S63924

A.Molecule type: DNA

A:Status: nucleic acid sequence not shown; translation not shown

A:Residues: 794-987 <VAF>

A:Cross-references: EMBL:X87941; NID:g886908; PIDN:CAA61193.1; PID:g886937

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995

C:Comment: Phosphofructokinase is composed of four alpha chains and four beta chains.

C:Genetics:

A:Gene: SGD:PFK1; MIPS:YGR240C

A:Cross-references: SGD:S0003472; MIPS:YGR240C

A:Map position: 7R

C:Superfamily: 6-phosphofructokinase, eukaryotic type; 6-phosphofructokinase 1 homology

C:Keywords: ATP, glycolysis, phosphotransferase

F:208-517/Domain: 6-phosphofructokinase 1 homology <6PF1>

F:596-886/Domain: 6-phosphofructokinase 1 homology <6PF2>

F:1225-229/Binding site: AMP, allosteric (Arg) #status predicted

F:309-310/Binding site: ATP (Asp, Gly) #status predicted

F:356/Active site: Asp #status predicted

F:398-455,482-488,491-729/Binding site: fructose-6-phosphate (Met, Glu, Lys, His, Arg, C

F:751/Binding site: citrate, allosteric (Lys) #status predicted

Query Match 10.8%; Score 246.5; DB 1; Length 987;

Best Local Similarity 23.9%; Pred. No. 1.8e-09;

Matches 103; Conservative 68; Mismatches 135; Indels 125; Gaps 19;

```

QY 31 KPKVAVITAGGLPCNSAIGSLERTEIDPSIETICRYGKGLLGDSYPTAVR 90
DB 204 KKKKIAVNTSGDSGMMAVRAVR--TGHFGDVFAYRGGGLRGKTY---LK 256
QY 91 KKA-----GVLQRFQSVIGNSRVKLTNVKDCVKGKEDPQKVAADQLVGDYDIL 145
DB 257 KMAEDVAVGMLSE--GGTLIGTA-----RSMFRREBERGQAAGMLISGIDAL 303
QY 146 HTIGDDPTNTAAAL-----AFLARNTY-----GLTVIGLPTVNDVPEPI 187
DB 304 VVCGDGSGLT--GADLPHEWPSLVDELVAEGRFKEVAPYKRLISVGLVGSINDMSGT 362
QY 188 KQSLGAMTAAEQAGRYFENNVAAENNAAPMLIVHVGRCNGMTL---ATAOEYRKL 243
DB 363 DSTIGAVSALERICEMVDYIDATKSHSRAPV--EVNGRHCGMLAAMGATGADY---- 417
QY 244 DRAEMLPELGLTRESYVAVFVPEADILAEAKRIAEVMDKDCV----NIFVSEGA 298
DB 418 -----IFPERAVPFGKMODEKEVQORHRSKGRNNITIVAEGA 457
QY 299 -----GVEATVAEQAKQOEVRDAFGHIK--DAVNGCKMFGEGEPAMIGAEK 345
DB 458 LDDQANVTYANDVDALIEL---GLDTKYVITLGHVQGGAGVAVADRLAT--LOGVDAYK 512
QY 346 TLVQKSGYPAPASNN-----VDDNRLIKSCADLAVECAFRESGVIGHDE 391
DB 513 AYLE---FTPEPSPILIGILENKIIRMPVSEVYKLTLSVA-----TAIENKDF 557
QY 392 DNGNVLAIEF 402
DB 558 DKALSLDTEP 568

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RESULT 11

S32902


```

QY 83 YPVTAEVRKAGVLAGRFSGVIGNSRVKLTNVADCVKRGVKEGEDPOKVAADQVYKDV 142
DB 66 SKVEITDSVSRKIHGEGSLTKTSRANP-----KQEDLQRY-VKQLOKQEV 113
QY 143 DLIHTIGGDDTNTAAADLAFLARNYGLTVGLPTVNDVFPRIKSL---GAMTAEQ 199
DB 114 SILVITIGDD--TAFSSMSVAKAANN-ELHVCHVPTINDL-PLVYGFPTGYETARBF 169
QY 200 GARFENNVAAENNANRMLIVHEVNGRNGMLT---AATPOEYKLLDAEWLPELGLTR 256
DB 170 GANVENLMTDASTASRYFIV-VAMGRQGHLAGIGKAGSHTLIPR-EZLP-----TT 223
QY 257 ESEYVAVE--VPEMAIDPEAS-AKRLREVMKVDQVNIFFSAGAVEAIVAM-QAKGQ 312
DB 224 DSEPEVTSRICDM---IEASITKRL--YTSKQGHVIVLEEGLEETVSTBELKQAFS 278
QY 313 EYPRDAFGHITKLDANVPKWFGEQFAQMT---GAETLVOKS-GYPARASASNVDMRLI 368
DB 279 SLKYDADHIMLAELDFGLVDEMEERMRRLKIAFTEKMGYELACAPENAFDREYV 338
QY 369 KSCADLAVECAPRRESGVGHEDNGNVLRALIEPRIRKGL--PRNIDTWNLSLSEIG 426
DB 339 RDLGNARVYLLANGNGAL-----ITVGVKNVPLSPD-----DLK 374
QY 427 QPKGK-----VEVS 436
DB 375 DPTGKTPTROVDVS 389

```

RESULT 14

6-phosphofructokinase [imported] - Salmonella enterica subsp. enterica serovar Typhi (st 6-phosphofructokinase enterica subsp. enterica serovar Typhi
A:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 12-May-2003
C:Accession: AH0942
R:Parthill, U.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, C.; T. Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Mould, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Nature 413, 848-852, 2001
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0942
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <PAR>
A:Cross-references: GB:AF513382; PIDN:CAD09562.1; PID:g16504676; GSPDB:GN00176
C:Genetics:
A:Gene: STY3809
C:Superfamily: 6-phosphofructokinase, bacterial type; 6-phosphofructokinase 1 homology

```

Query Match 10.5%; Score 240.5; DB 2; Length 320;
Best Local Similarity 24.8%; Pred. No. 1e-09;
Matches 102; Conservative 59; Mismatches 122; Indels 129; Gaps 18;
QY 33 KKVAILTAGGLAPCLNSAIGSLIERYTEIDPSIETICRYGKGL-----LLGDSYPTVA 87
DB 3 KKGIVLTSGGDAPGNNAAIRGVVR--AALTEGLEWGIYDGLYEDRWVQLDRYSVD 60
QY 88 EVRKAGVLAGRFSGVIGNSRVKLTNVADCVKRGVKEGEDPOKVAADQVYKDVILHT 147
DB 61 MINR-----GGFPLSAR--PEPRD-----ENIRVALENKKRISIDLVV 100
QY 148 IGGDDTNTAAADLAFLARNYGLTVGLPTVNDVFPRIKSLGAMTAEQARFENV 207
DB 101 IGGDSYVGAARL-----TEGFPICIGLPGTINDIGCTGYTTCYFALGTVBAIDL 154
QY 208 VAENNANRMLIVHEVNGRNGMLTAAQGYRKLDAEWL--PELGLTRESYVAVF 265
DB 155 RDTSSSHORISIV-EVMGRYCGDLTLAA-----IAGCEPIVVEVEFNRB----- 200
QY 266 VPEMAIDPEAEAK-----RLREWMDKVDQVNIFFSAGAVE--AIVAEQAK 310

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DB 201 -----DLVAETKAGIANGKRAIVALTEHMDVDVLAHFIEKRGRETRATVLAGHIG 254
QY 311 GQVEPRDAFGHITKLDANVPKWFGEQFAQMTGAETLVOKSGYFARASASNVDMRLIS 370
DB 255 GSPFVYD-----RILSRGAYV----- 272
QY 371 CADLAVE-----CAFRRESVIGHEDNGNVLRALIEPRIRKGLKPNIDTW 417
DB 273 -IDLILBEHGRGCVGIGQNEQLVHD-----IIDALENRK-----RPFK--SDW 312

```

RESULT 15

6-phosphofructokinase (EC 2.7.1.11) 1 - Escherichia coli (strain K-12)
N:Alternate names: phosphofructokinase 1, isozyme 1, phosphohexokinase, isozyme 1
C:Species: Escherichia coli
C:Date: 31-Dec-1968 #sequence_revision 10-Oct-1997 #text_change 12-May-2003
C:Accession: G65197; A25206; S40859
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C. A.; Rose, D.U.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G65197
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-320 <BLAT>
A:Cross-references: GB:AE000466; GB:U00096; NID:G2367328; PIDN:AACT6898.1; PID:g1790350;
A:Experimental source: strain K-12, substrain MG1655
R:Hellenga, H.W.; Evans, P.R.
Eur. J. Biochem. 149, 363-373, 1995
A:Title: Nucleotide sequence and high-level expression of the major Escherichia coli pho
A:Reference number: A91144; MUID:85203917; PMID:3158524
A:Accession: A25206
A:Molecule type: DNA
A:Residues: 1-73, 'C', 75-102, 'DG', 105-162, 'P', 164-316, 'E', 318, 'W', 320 <HEL>
A:Cross-references: GB:X02519; NID:g42365; PIDN:CAM26356.1; PID:g42366
A:Note: This sequence has since been corrected
R:Evans, P.R.
submitted to the EMBL Data Library, October 1986
A:Reference number: A94501
A:Contents: annotation; corrections
R:Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 21, 3391-3398, 1993
A:Title: Analysis of the Escherichia coli genome. III. DNA sequence of the region from 8
A:Reference number: S40802; MUID:9347969; PMID:8346018
A:Accession: S40859
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-320 <PLU>
A:Cross-references: EMBL:L19201; NID:g304961; PIDN:AAE03048.1; PID:g305019
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993
C:Comment: The active enzyme catalyzes the key control step of glycolysis, the phosphory
Y ADP and inhibited by phosphoenolpyruvate.
C:Comment: In E. coli this enzyme is responsible for 90% of the phosphofructokinase acti
vities are different kinetically; there is also no immunological cross-reactivity.
C:Genetics:
A:Gene: pfkA
A:Map position: 88 min
C:Superfamily: 6-phosphofructokinase, bacterial type; 6-phosphofructokinase 1 homology
C:Keywords: allosteric regulation; ATP; homotetramer; phosphotransferase
F/5-279/Domains: 6-phosphofructokinase 1 homology <6PFI>

```

Query Match 10.4%; Score 238.5; DB 1; Length 320;
Best Local Similarity 24.9%; Pred. No. 1.4e-09;
Matches 100; Conservative 65; Mismatches 132; Indels 105; Gaps 18;
QY 33 KKVAILTAGGLAPCLNSAIGSLIERYTEIDPSIETICRYGKGL-----LLGDSYPTVA 87
DB 3 KKGIVLTSGGDAPGNNAAIRGVVR--AALTEGLEWGIYDGLYEDRWVQLDRYSVD 60
QY 88 EVRKAGVLAGRFSGVIGNSRVKLTNVADCVKRGVKEGEDPOKVAADQVYKDVILHT 147

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Db      61 MINR-----GTFSSAR--FPERD-----ENIRAVAIENLKKRGIDALV 100
Qy      148 IGGDDPTTAADLAFLARNNYGLTVIGLPTVDNDVEPIKOSLGAWTAAEQARYFMNV 207
Db      101 IGGDGSYMGAMRL-----TEWGFPCIGLPGTIDNDIKGTDYTIQFTALSTVVEAIDRL 154
Qy      208 VAENNANPRMLIVHEVMGRNCGMLTAATQOEYRKLLDRAEW--LPELGITRESYEVHAF 265
Db      155 RDTSSSHQRIISV--EWMGRYCGDLTLAA-----LAGCEPVVVEVERFRED-----L 202
Qy      266 VPEMAIDLEAEKR-----LREWMDKVDGVNIFVSBGAVE---AIVAMQAKQOEYPRD 317
Db      203 VNEIKAGI-AKQKKEAIVAITHEMCDVDELANFIKGTGRETRATVGHIOGGSPPVYD 261
Qy      318 AFGHIKLDVAVNPGKWFGEQFQOMIGAETLVOKSGYFAPASASVNDMRLIKCADLAVB 377
Db      262 RI-----LASRMGAVAIIDLILAGYGR----- 283
Qy      378 CAFRESGVIGHDEDNVTLRAIEPPIKGGKPPNIDTWFN 419
Db      284 CVGIONEQLVHND-----IIDAIENMK---RPFK--GDWLD 314

```

Search completed: January 29, 2004, 14:38:27
 Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 14:08:27 ; Search time 17 Seconds

(without alignments)
1208.863 Million cell updates/sec

Title: US-09-941-947a-2

Perfect score: 2284

Sequence: 1 DVVTWYHITADIRCHWTF.....FNSMLSEIQPKGNVSH 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1314	57.5	403 1	PPF_PROPR
2	311	13.6	342 1	K6P1_STRCO
3	305	13.4	346 1	PPF_DICTH
4	298.5	13.1	341 1	PPF_AMYMB
5	281.5	12.3	341 1	K6P1_STRCO
6	274.5	12.0	341 1	PPF_AMYMB
7	271.5	11.9	341 1	K6P1_STRCO
8	253	11.1	319 1	K6P1_THEMA
9	246.5	10.8	367 1	K6P1_YEAST
10	245.5	10.7	992 1	K6P1_KUOLA
11	242	10.6	319 1	K6P1_CLOPE
12	240.5	10.5	320 1	K6P1_SALTY
13	238.5	10.4	320 1	K6P1_ECOLI
14	234.5	10.3	327 1	K6P1_YERPE
15	233.5	10.2	322 1	K6P1_BACMC
16	233	10.2	319 1	K6P1_LACDE
17	230	10.1	322 1	K6P1_FUSNN
18	229.5	10.0	320 1	K6P1_ENTCL
19	226	9.9	322 1	K6P1_THETH
20	224.5	9.8	329 1	K6P1_DEIRA
21	223.5	9.8	319 1	K6P1_BACBD
22	223.5	9.8	320 1	K6P1_BUCBP
23	223.5	9.8	320 1	K6P1_VIBCH
24	223	9.8	343 1	K6P1_MYCTO
25	222	9.7	340 1	K6P1_LACLA
26	222	9.7	320 1	K6P1_YARLI
27	220.5	9.7	320 1	K6P1_BUCAP
28	220	9.6	779 1	K6P1_RABIT
29	216.5	9.5	319 1	K6P1_CIOAB
30	216	9.5	337 1	K6P1_STRP8
31	216	9.5	337 1	K6P1_STRP8
32	216	9.5	337 1	K6P1_STRPY
33	216	9.5	784 1	K6P1_MOUSE

34	215	9.4	335 1	K6P1_STRPN	Q97rc6 streptococ
35	214.5	9.4	339 1	K6P1_STRTR	Q919e3 streptococ
36	213.5	9.3	321 1	K6P1_AQUAE	O67605 aquifex aeo
37	213.5	9.3	775 1	K6P2_ASFOR	Q9b920 aspergillus
38	212	9.3	781 1	K6P1_CANPA	P52784 canis famli
39	211	9.2	779 1	K6P1_MOUSE	P47857 mus musculu
40	210.5	9.2	320 1	K6P1_BUCAI	P57391 buchnera ap
41	210.5	9.2	343 1	K6P1_MYCIB	O33106 mycobacteri
42	210	9.2	779 1	K6P1_HUMAN	P08237 homo sapien
43	210	9.2	789 1	K6P1_HABCO	Q27665 haemophilus
44	210	9.2	987 1	K6P1_CANAL	O94201 candida alb
45	209	9.2	319 1	K6P1_BACST	P00512 bacillus st

ALIGNMENTS

RESULT 1
PPF_PROPR STANDARD; PRT; 403 AA.

AC P29495;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyrophosphate--fructose 6-phosphate 1-phosphotransferase (EC 2.7.1.90)
DE (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-
DE dependent 6-phosphofructose-1-kinase) (PFI-dependent
DE phosphofructokinase) (PFI-PFK).
GN PPF OR PFK.
OS Propionibacterium freudenreichii shermanii.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Propionibacteriaceae; Propionibacteriaceae; Propionibacterium.
OX NCBI_TaxID=1752;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91358443; PubMed=1653240;
RA Lador U.S., Gollapudi L., Tripathi R.L., Latschaw S.P., Kemp R.G.;
RT "Cloning, sequencing, and expression of pyrophosphate-dependent
RT phosphofructokinase from Propionibacterium freudenreichii."
RL J. Biol. Chem. 266:16550-16555(1991).
RN [2]
RP IDENTIFICATION OF CRITICAL LYSYL RESIDUES.
RX MEDLINE=92273593; PubMed=117210;
RA Green P.C., Latschaw S.P., Lador U.S., Kemp R.G.;
RT "Identification of critical lysyl residues in the pyrophosphate-
RT dependent phosphofructo-1-kinase of Propionibacterium
RT freudenreichii."
RL Biochemistry 31:4815-4821(1992).
RU Biochemistry 31:4815-4821(1992).
CC -1- CATALYTIC ACTIVITY: Diphosphate + D-fructose 6-phosphate =
CC phosphate + D-fructose 1,6-bisphosphate.
CC -1- ENZYME REGULATION: NON-ALLOSTERIC.
CC -1- PATHWAY: Key control step of glycolysis.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOFRUCTOKINASE FAMILY. PPF
CC SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL collaboration
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb.ch/announce/>
CC or send an email to license@isb.ch).
CC -----
CC EMBL: M67447; AAA25675.1; -
CC PIR: A41169; A41169.
CC InterPro: IPR000023; Pfrckinase.
CC Pfam: PF00365; PFK.1.
CC PRINTS: PR00476; PFRCKTKINASE.
CC ProDom: PD000707; Pfrckinase.1.
CC Transferrase; Kinase.
CC INIT MET 0
CC NP_BIND 120 125 PYROPHOSPHATE (POTENTIAL).
CC FT

FT ACT_SITE 150 150 NUCLEOPHILE (POTENTIAL).
 SQ SEQUENCE 403 AA; 43114 MW; 1DED3272BA42B6E6 CRC64;
 Query Match 57.5%; Score 1314; DB 1; Length 403;
 Best Local Similarity 62.6%; Pred. No. 1.2e-81;
 Matches 248; Conservative 60; Mismatches 88; Indels 0; Gaps 0;

QY 33 KVAITAGLAPCLNSAIGSLERTYEIDPSIRIICRGYKGLLGDSPVTAVERKK 92
 DB 2 KKAVALTAGGAPCLNSAIGSLERTYEIDPSIRIICRGYKGLLGDSPVTAVERKK 61
 QY 93 AGVLOREGVGNSRYKLVNVDQVKGGLVKEGEPQKAAQGLVMDGDIHTIGSD 152
 DB 62 YDPLFSGSGSPIGSKVLTNVDLVARGLVAGSDOPLKAAQGLVMDGDIHTIGSD 121
 QY 153 TMTAADLAAFLARNNYGLTVIGLPTVNDVFPKISGLGAWTAQAGARYFNVAERN 212
 DB 122 TMTAADLAAFLARNNYGLTVIGLPTVNDVFPKISGLGAWTAQAGARYFNVAERN 181
 QY 213 ANRMLIVHEWGRNGMTLTAATQAEYKLLDPAEMLPELGLTRESYEVHAAVPEMAID 272
 DB 182 AAFRELIHEWGRNGMTLTAATQAEYKLLDPAEMLPELGLTRESYEVHAAVPEMAID 241
 QY 273 LESAARGLREWMDKVDQCNIFVSEAGVBAIVAEQAGQEVPRDAFGHILDAVNPGRK 332
 DB 242 LDEAEERLRTVMDQVGSVNFISEGAGVPDVAQMGATGQEVPTDAFGHVDKINPGAM 301
 QY 333 FGSQFPAQMTGAKETLVQKSGYFPAASAVNDKRLIKSCADLAECQAFRESGVIGHED 392
 DB 302 FASQFPAQMTGAKETLVQKSGYFPAASAVNDKRLIKSCADLAECQAFRESGVIGHED 361
 QY 393 NGAVLRAIFERRIKGKGFNIDTDMWNSMLSEIGOP 428
 DB 362 AGDKLVITDKRIAGHKFPDITDWTYQTLARIGOP 397

RESULT 2
 K6P1_STRCO STANDARD; PRT; 342 AA.
 AC 008333;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 6-phosphofructokinase 1 (EC 2.7.1.11) (Phosphofructokinase 1)
 GN (Phosphofructokinase 1) (ATP-PFK).
 DN PFKA1 OR PFKA OR PFK1 OR SC02119 OR SCGE10.13C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae;
 OC Streptomycetaceae; Streptomycetes.
 ON NCBI_TaxID=1902;
 RX MEDLINE=97208211; PubMed=9055413;
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=A3(2) / 1109;
 RA MEDLINE=97208211; PubMed=9055413;
 RA Alices A.M.C.R., Euvierink G.U.W., Bibb M.J., Dijkhuizen L.;
 RT Identification of ATP-dependent phosphofructokinase as a regulatory
 step in the glycolytic pathway of the actinomycete Streptomyces
 coelicolor A3(2).
 RL Appl. Environ. Microbiol. 63:956-961 (1997).
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21964410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabbittowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares K., Squares S., Taylor K.,
 RA Warren T., Wierozorek A., Woodward J., Barrett B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2).
 RL Nature 417:141-147 (2002).
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
 CC fructose 1,6-bisphosphate.
 CC -1- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY
 CC PHOSPHOENOLPYRUVATE.
 CC -1- PATHWAY: Key control step of glycolysis.
 CC -1- SUBUNIT: Homotetramer (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
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 CC -----
 DR EMBL: U51728; AAC45135.1; -.
 DR EMBL: AL938111; CAB51967.1; -.
 DR PIR: T35500; T35500.
 DR HSSE: P00512; 3PFR.
 DR HAMAP: MF_00339; -; 1.
 DR InterPro: IPR000023; Pfrfructokinase.
 DR Pfam: PF00365; PFR; 1.
 DR PRINTS: PR00476; PFRCTKINSE.
 DR ProDom: PD000707; Pfrfructokinase.
 DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
 DR KX Kinase; Transferrase; Glycolysis; Multigene family; Allosteric enzyme;
 KW Complete proteome.
 SQ SEQUENCE 342 AA; 36664 MW; CEEFC7B74092AB34 CRC64;
 Query Match 13.6%; Score 311; DB 1; Length 342;
 Best Local Similarity 27.4%; Pred. No. 5.1e-14;
 Matches 105; Conservative 63; Mismatches 137; Indels 78; Gaps 17;

QY 34 KVAITAGLAPCLNSAIGSLERTYEIDPSIRIICRGYKGLLGDSPVTAVERKK 93
 DB 2 KVAITAGLGDQCGNLAIVARVARKGV-QYGVDFGFGPDGMRGLBGTVL-DIPAVR 58
 QY 94 GYLORFGGSVIGNSVYKLTNVDQVKGGLVKEGEPQKAAQGLVMDGDIHTIGSD 153
 DB 59 GILPR-GGVVLAGSSRTNPKQKRDGIRK-----IKDNLAALGVEALITYIGEDT 105
 QY 154 NTPAADLAAFLARNNYGLTVIGLPTVNDVFPKISGLGAWTAQAGARYFNVAERN 213
 DB 106 LGVATRLA-----DEYGVPCGVGERTINDLSAIDYTGDPDTAGIATEAIDRLHTTAS 160
 QY 214 NPMRLIVHEWGRNGMTLTAATQAEYKLLDPAEMLPELGLTRESYEVHAAVPEMAID 273
 DB 161 HMRVLIVV-EVWGRHAGTALHS-----GLAGCA---NVILIPQRPDV 199
 QY 274 EA-----EAKRLREWMDKVDQCNIFVSEAGVBAIVAEQAGQEVPR-----DAFGHILKD 325
 DB 200 BOVCQWTSRFRASAPV-----VVABGA-----MFRGDMVLKQESLDSYHVALS 247
 QY 326 AVNPKMGEGQPAQMTGAE-KTLVQKSGYFPAASAVNDKRLIKSCADLAECQAFRES 384
 DB 248 GV--GEMLAKQIBKRTGNEARTTV--LGHVQRGGTPSAFDRMLATRFGLHAVDV----- 298
 QY 385 GVIGHEDENGV--LRALFPR 405
 DB 299 ---HDGDFGKVALRGTDIVRV 317

RESULT 3
 ID_PFP_DICTH STANDARD; PRT; 346 AA.
 AC 09K471;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

D3 Pyrophosphate--fructose 6-phosphate 1-phosphotransferase (EC 2.7.1.90)
D3 (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-
D3 dependent 6-phosphofructose-1-kinase) (Ppi-dependent
D3 phosphofructokinase) (Ppi-PFK).
OS Bacterioides thermophilum.
OC Bacterioides thermophilum; Dictyoglomales; Dictyoglomaceae; Dictyoglomus.
OX NCBI_TaxID=14;
RN PFP.
RP SEQUENCE FROM N.A.
RC STRAIN=RC46 B.1;
RX MEDLINE=20372656; PubMed=10913106;
RA Ding Y.-H.R., Rommus R.S., Morgan H.W.,
RT "Sequencing, cloning, and high-level expression of the pfp gene,
RT encoding a ppi-dependent phosphofructokinase from the extremely
RT thermophilic eubacterium Dictyoglomus thermophilum.";
RL J. Bacteriol. 182:4661-4666(2000).
CC -i CATALYTIC ACTIVITY: Diphosphate + D-fructose 6-phosphate =
CC phosphate + D-fructose 1,6-bisphosphate.
CC -i PATHWAY: Key control step of glycolysis.
CC -i SIMILARITY: Belongs to the phosphofructokinase family.
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CC
CC EMBL: AF568276; AAF80100.1;
DR HSSP: P06998; 2PKF.
DR HAMAP: MF_00339; -; 1.
DR InterPro: IPR000023; Pfruckinase.
DR Pfam: PF00365; PFK; 1.
DR PRINTS: PR00476; PFRCTKINASE.
DR PRODOM: PD000707; Pfruckinase.
DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; FALSE_NEG.
KW Kinase; Transferase; Glycolysis.
SQ SEQUENCE 346 AA; 37448 MW; 50C03B64BA7927F1 CRC64;
Query Match 13.4%; Score 305; DB 1; Length 346;
Best Local Similarity 27.5%; Pred. No. 1.3e-13;
Matches 107; Conservative 73; Mismatches 155; Indels 54; Gaps 15;
QY 34 KVALITAGGLAPCLNSAIGSLIERYTEIDPSIEIICRYGKGLLGDSPYVTAVERKKA 93
DB 5 RIGVLTGGGDCPGLNPAIRGIWMR-ALDYDEVITGLKYGWAGLLKADYPLSLEWED- 61
QY 94 GVLORFGSGVIGNSRVKLTNVKDCVKGGLVKEGDPQKAVADQLVKGVDIILHTIGDDT 153
DB 62 --LIEIGTILGSSR---TNP-----FKCEDVYK-CYENFKKNTLDALLIIGSEDT 107
QY 154 NTAADLAALFLARNNGYGLTVIGLPTVNDVFPPIKOSIGANTAAEGARVPNNVAENNA 213
DB 108 LGVASKP-----SKGLPMTIGVPTKIDKOLEEDTDTGFTAVEVVDAIKRLDPTARS 161
QY 214 NPMRLIVHEVNGRNGCMLTAATAQRYKLLDRAEMLPGLITRESYEVNAVPEMAIDL 273
DB 162 HARIIV-ELMGRAGMAL-----YGLAGADY-----LILPEVAPNL 200
QY 274 EAEAKRLREVMNDK-VDCVNI FVSEAGVEAIVAEQAKGQEVPRDAFGHIKLDVNGKMP 332
DB 201 EDLVNHLRKLYARGRNNAVAIAEGVOLPGFTYQ--KQEGMWDAGHIRLGGV--GNV 255
QY 333 FGEQFAMIGAEKTLVQSGVPAASASNDPMRLISCDLAECAFRRESGVIGHDED 392
DB 256 LAEITQKNGIETRAVILS-HLQFGSGPSIRDRIMGLLKGKAVDLVBEKSGLF--VAV 312
QY 393 KGNVLAIEEPRIRKGPFPNIDTWMNSM 421
DB 313 KGNELVAVDITLIE-GTKKVDPAFESSV 340

RESULT 4
PFP AMYME STANDARD; PRT; 341 AA.
AC Q59126;
DT 15-JUN-1998 (Rel. 36, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyrophosphate--fructose 6-phosphate 1-phosphotransferase (EC 2.7.1.90)
DE (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-
DE dependent 6-phosphofructose-1-kinase) (Ppi-dependent
DE phosphofructokinase) (Ppi-PFK).
OS Amycolatopsis methanolic.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiales; Pseudonocardaceae; Amycolatopsis.
OX NCBI_TaxID=1814;
RN PFP.
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96125240; PubMed=8550409;
RA Alves A.M., Meijer W.G., Vrijbloed J.W., Dijkhuizen L.;
RT "Characterization and phylogeny of the pfp gene of Amycolatopsis
RT methanolica encoding ppi-dependent phosphofructokinase.";
RL J. Bacteriol. 178:149-155(1996).
CC -i CATALYTIC ACTIVITY: Diphosphate + D-fructose 6-phosphate =
CC phosphate + D-fructose 1,6-bisphosphate.
CC -i PATHWAY: Key control step of glycolysis.
CC -i SUBUNIT: Homotetramer.
CC -i SIMILARITY: Belongs to the phosphofructokinase family.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U31277; AAB01683.1; ALT_INIT.
DR HSSP: P00512; 3PFX.
DR HAMAP: MF_00339; -; 1.
DR InterPro: IPR000023; Pfruckinase.
DR Pfam: PF00365; PFK; 1.
DR PRINTS: PR00476; PFRCTKINASE.
DR PRODOM: PD000707; Pfruckinase; 1.
DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
KW Kinase; Transferase; Glycolysis.
SQ SEQUENCE 341 AA; 36229 MW; 306613246172D36B CRC64;
Query Match 13.1%; Score 298.5; DB 1; Length 341;
Best Local Similarity 28.8%; Pred. No. 3.5e-13;
Matches 108; Conservative 59; Mismatches 147; Indels 61; Gaps 16;
QY 34 KVALITAGGLAPCLNSAIGSLIERYTEIDPSIEIICRYGKGLLGDSPYVTAVERKKA 93
DB 2 RIGVLTGGGDCPGLNPAIRGIWMR-ALDYDEVITGLKYGWAGLLKADYPLSLEWED- 61
QY 94 GVLORFGSGVIGNSRVKLTNVKDCVKGGLVKEGDPQKAVADQLVKGVDIILHTIGDDT 153
DB 60 --LIEIGTILGSSR---TNP-----FKCEDVYK-CYENFKKNTLDALLIIGSEDT 107
QY 154 NTAADLAALFLARNNGYGLTVIGLPTVNDVFPPIKOSIGANTAAEGARVPNNVAENNA 213
DB 106 LGVASKL-----TDGIGVGVPTKIDNDLAATDTGFTDAVNHATEAIDRLRTARS 159
QY 214 NPMRLIVHEVNGRNGCMLTAATAQRYKLLDRAEMLPGLITRESYEVNAVPEMAIDL 273
DB 160 HARIIV-ELMGRAGMAL-----YGLAGADY-----LILPEVAPNL 200
QY 274 EAEAKRLREVMNDK-VDCVNI FVSEAGVEAIVAEQAKGQEVPRDAFGHIKLDVNGKMP 333
DB 199 EGVNEMVERFERKMTAPIIVAEAGVPRG-GAEVLRGTS---KDAFGHQLGCV--GTWL 252

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QY 334 GEGPOMIGAKTIVOKSGYFAPASASNDMDRLIKSCADLAVECAFRESGVIHDEDN 333
DB 253 ADEIAERTGESSRAV-VLGHGTGRTPTAYDRVLATFGLHAYDAV-----ADGDF 302
QY 394 GNV--LRAIEPRRIK 406
DB 303 GTWVALRGTDIVRVK 317

RESULT 5
K6P3_STRCO
ID K6P3_STRCO STANDARD; PRT; 341 AA.
AC Q9RC99;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphofructokinase 3 (EC 2.7.1.11) (Phosphofructokinase 3)
GN PFKA3 OR PFK3 OR SC01214 OR 2SCG58.14.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.B., James K.D., Harris D.B., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RA "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -|- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -|- PATHWAY: Key control step of glycolysis.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: Belongs to the phosphofructokinase family.
CC
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CC
CC EMBL: AL939108; CAC01496.1; -
CC HSSP: P00512; 3PFK.
CC HAMAP: MF_00339; -; 1.
CC InterPro: IPR000023; Pffrckinase.
CC Pfam: PF00365; PFK; 1.
CC PRINTS: PR00476; PHFRCKINASE.
CC ProDom: PD000707; Pffrckinase; 1.
CC PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
CC KINASE, Transferase; Glycolysis; Multigene family; Complete proteome.
SQ SEQUENCE 341 AA; 36431 MW; E3050D37BDE6F9F0 CRC64;

Query Match 12.3%; Score 281.5; DB 1; Length 341;
Best Local Similarity 26.8%; Pred. No. 5e-12;
Matches 100; Conservative 66; Mismatches 152; Indels 55; Gaps 12;
QY 34 KVALILANGELAPLNAIGSLIRRYEIDPSIITCYRGYKULLGDSYPTAERKKA 93
DB 2 RIVGLTSGGECPLNANIRSVAR-AVVDHGDVIGFRGWMKLLGCDY--LKLDDAVG 58
QY 94 GVLGRSGVIGNSRVLTIVKDCVKGDEDEQKVAADQVLVDGVDLHTTGIDDT 153

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DB 59 GILAR-GGITLIGSSVPRPEHLRDGVER-----ARGVIELGIDALIPIGEGGT 105
QY 154 NTPAADLAALFARNYVGLVIGLPTKVDVFPPIKQSGAMTAAEGAGYFNNVAENNA 213
DB 106 LKARALL-----SDNGLPVGVPTINDVDVTDVTFGPTAVVATALRLKTTAS 159
QY 214 NPMPLIVHEVMGRNGCMTLAAVQAEYRKLLDRAEWLPELGLTRESYEAIVPEMALDL 273
DB 160 HORVLIV-EVMGRHGMIALHSGM-----AAGAAVAVVPERPFDI 198
QY 274 EAEAKRLPEVMKVDVNVLPV-SBGAQVATYAEQAGQEVPRAPFGHILKLDVAVRGSM 332
DB 199 DELTAKVGRFSAGRFAIIVAAGAKKAGTMDDEG---KUYGHERPAGI--ARQ 252
QY 333 FEGPOMIGAKTIVOKSGYFAPASASNDMDRLIKSCADLAVECAFRESGVI---G 388
DB 253 LSELIERLGRKARV-ILGHVGRGTPTAYDRVLATFGHVAVEAVHGRGFKYATLRG 311
QY 389 HDEDNGNVLRALTE 401
DB 312 TDIEVWSIADAVE 324

RESULT 6
PFP_AMYMD
ID PFP_AMYMD STANDARD; PRT; 341 AA.
AC Q9AGC0;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyrophosphate--fructose 6-phosphate 1-phosphotransferase (EC 2.7.1.90)
DE 6-phosphofructokinase, pyrophosphate dependent (Pyrophosphate-
DE dependent 6-phosphofructose-1-kinase) (Ppi-dependent
DE phosphofructokinase) (Ppi-PFK).
GN PFP.
OS Amycolatopsis mediterranei (Nocardia mediterranei).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
OX NCBI_TaxID=33910;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S699;
RA Kuan L., Mueller M., August P.R., Pogosova-Agadjanyan E., Floss H.G.,
RA Yu T.;
RA "Characterization and cloning of three 3-deoxy-D-arabinopulosonate
RT 7-phosphate synthase isoenzymes from Amycolatopsis mediterranei
RT S699.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: Diphosphate + D-fructose 6-phosphate =
CC phosphate + D-fructose 1,6-bisphosphate.
CC -|- PATHWAY: Key control step of glycolysis.
CC -|- SUBUNIT: Homotrimer (By similarity).
CC -|- SIMILARITY: Belongs to the phosphofructokinase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF36847; AAK28147.1; -
CC HSSP: P00512; 3PFK.
CC HAMAP: MF_00339; -; 1.
CC InterPro: IPR000023; Pffrckinase.
CC Pfam: PF00365; PFK; 1.
CC PRINTS: PR00476; PHFRCKINASE.
CC ProDom: PD000707; Pffrckinase; 1.
CC PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
CC KINASE, Transferase; Glycolysis.
SQ SEQUENCE 341 AA; 36272 MW; 2B5C28E7BBD57065 CRC64;

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RT genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -1- PATHWAY: Key control step of glycolysis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
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CC
DR EMBL: AE001705; AAD5301.1; -.
DR PIR: C72406; C72406.
DR HSSP: P00512; 3PFK.
DR TIGR: TMO208; 3PFK.
DR HAMAP: MF_00339; -.
DR InterPro: IPR000023; Pfruckinase.
DR Pfam: PF00365; PFK.1.
DR PRINTS: PR00476; PFRCKTKINASE.
DR PRODOM: PD000707; Pfruckinase.
DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
DR KINASE: Transferase; Glycolysis; Complete proteome.
SQ SEQUENCE 319 AA; 34487 MW; 3809B97128BD1288 CRC64;

Query Match 11.1%; Score 253; DB 1; Length 319;
Best Local Similarity 26.6%; Pred. No. 3.9e-10;
Matches 95; Conservative 60; Mismatches 126; Indels 76; Gaps 14;

QY 33 KRAVITAGGLAPCLNSAIGSLIRTYEIDPSIEITCYRGYKGLLGDSYPTAYVRK 92
DB 2 KKAIVITSGDAGGMAAAYAV-RY-GVAGQLEIVGVRGSGLLDGF--VKLEKGV 57
QY 93 AGVLQFGSGVINSRVKLTNVDCVKGGLVKEGEPQKVAADQVKGVDIHTIGEDD 152
DB 58 AGITK-GGTILTSNCEFT-----EGRELAQAQIKGHIGLVIGSG 104
QY 153 TTTAAADLAAFLARNYGLTVIGLPTVNDVFPFQSLGAMTAAQAGARYFNVAERN 212
DB 105 SLT-----GAILLYEESHKLPVVGIPATIDMDIGLTDMCIGVDTCENTVMDAVOKLDTAS 159
QY 213 ANRPLIVHEVMGRNGCMTFAATAQERYKLDRAEMLPGLTRRESYEVHVAVPEMAID 272
DB 160 SHERATV-EVMGRHSGYIMLAG-----LYTGA-----AIVPEIPVD 198
QY 273 LEAEANRLREV--MDRYDCNIVFVSGAGVEAIVAEQAQAGVPPDAGHTLDAVNG 330
DB 199 YSOLADRIELEERRGRKINSI-IIVAEGASAYTVAR-----HLE----- 236
QY 331 KMGEGEAGNIGAKETLYQSGYFARASASNVDMILISCADLVECAFRPSSGYI 387
DB 237 -----YRTGYE-ERTITLGHVQSGSPFAPDRRLASMGVEAVDALDGEVDV 284

RESULT 9
K6P1_YEAST
ID K6P1_YEAST STANDARD; PRT; 987 AA.
AC P16861;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, last sequence update)
DT 15-SEP-2003 (Rel. 42, last annotation update)
DB 6-phosphofructokinase (alpha subunit (EC 2.7.1.11) (phosphofructokinase
DE 1) (Phosphohexokinase) (6PF-1-K alpha subunit)).
GN PFK1 OR YGR240C OR G8599
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=89378757; PubMed=2528496;
RA Heintsch J.J., Ritzel R.G., von Borsel R.C., Aguilera A.,
RA Rodicio R., Zimmermann F.K.;
RT "The phosphofructokinase genes of yeast evolved from two duplication
RT events";
RL Gene 78:309-321(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=97245298; PubMed=9090057;
RA Guerrero I., Azevedo D., Barreiros T., Rodrigues-Pousada C.;
RT "Sequencing of a 9.9 kb segment on the right arm of yeast chromosome
RT VII reveals four open reading frames, including PFK1, the gene coding
RT for succinyl-CoA synthetase (beta-chain) and two ORFs sharing
RT homology with ORFs of the yeast chromosome VIII.";
RL yeast 13:275-280(1997).
RN [3]
RP SEQUENCE OF 794-987 FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=96267763; PubMed=8701610;
RA van der Aart Q.U.M., Kleine K., Steensma H.Y.;
RT "Sequence analysis of the 43 kb CRM1-YLM9-BT54-DIE2-SM11-PHO81-YHD4-
RT PFK1 region from the right arm of Saccharomyces cerevisiae chromosome
RT VII.";
RL Yeast 12:385-390(1996).
CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -1- ENZYME REGULATION: Allosterically inhibited by ATP and activated
CC by AMP and fructose 2,6-bisphosphate (By similarity).
CC -1- PATHWAY: Key control step of glycolysis.
CC -1- SUBUNIT: Heterodimer of 4 alpha and 4 beta chains.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the phosphofructokinase family. Two domains
CC subfamily.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: M26943; AAA34859.1; -.
DR EMBL: Z73025; CA97268.1; -.
DR EMBL: X87941; CA61193.1; -.
DR PIR: JQ0016; JQ0016.
DR HSSP: P00512; 3PFK.
DR SGD: S0003472; PFK1.
DR GO: GO:0005945; C:6-phosphofructokinase complex; IMP.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR GO: GO:0003872; F:6-phosphofructokinase activity; IMP.
DR InterPro: IPR00023; Pfruckinase.
DR Pfam: PF00365; PFK.2.
DR PRINTS: PR00476; PFRCKTKINASE.
DR PRODOM: PD000707; Pfruckinase; 2.
DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 2.
DR KINASE: Transferase; Glycolysis; Repeat; Allosteric enzyme.
SQ SEQUENCE 987 AA; 107970 MW; 995B3DFC7781B29 CRC64;

Query Match 10.8%; Score 246.5; DB 1; Length 987;
Best Local Similarity 23.9%; Pred. No. 4.3e-09;
Matches 103; Conservative 68; Mismatches 135; Indels 125; Gaps 19;

QY 31 KKKVAVITAGGLAPCLNSAIGSLIRTYEIDPSIEITCYRGYKGLLGDSYPTAYVR 90
DB 204 KKKKIAVWTSGDSDGMAAAYAVR--TGTHFGCDVAVVAGYGLLRGKXK-----LK 256
QY 91 KKA-----GVLRQFGSVTGNRVKLTNVDCVKGGLVKEGEPQKVAADQVKGVDI 145
DB 257 KKAIVITSGDAGGMAAAYAVR--TGTHFGCDVAVVAGYGLLRGKXK-----LK 303

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QY 146 HTIGEDDTNTAAADL-----AAFLARNY-----GLTVIGLPTKVDNDVPPI 187
 DB 304 VVCGGDGSLT-CHDLFRHEWPSIVDELVAEGRTKEEVAAPYKSLVGLVSDIDMDSGT 362
 QY 188 KOSLGAMTAEGAGRYEMVAVENNANPMLIVHEWGRNCWLT-----ATAQOEYKLL 243
 DB 363 DSTIGAYSLERICEMWDYIDATAKSHSAFVY-EVWGHCGLMLMGIALGADY---- 417
 QY 244 DDAEMLPGLTRRESYEVAVPEPMALILEAKRLREVMKVCV-----NIVYSGA 298
 DB 418 -----IFIPERAVPHGKQDELEKVCQRHSKGRNNITIVAGGA 457
 QY 299 -----GVEAIVAEWQKQGEVPRDAFHIKL--DAVNPQKPGQEPQMGIGAEK 345
 DB 458 LDDQNPVTANVYKALIEL---GLDTKTLIGHVQGGTAVAHDRMLAT--LQGVDAVK 512
 QY 346 TVQKSGYAPASASN-----VDMKRLKSCADLAVECAFRESGVIGDE 391
 DB 513 AVLE-----FTPEPSPILIGLENKILRMPLVESVGLTKSVA-----TALENDP 557
 QY 392 DNGNVLRAIEF 402
 DB 558 DKALISLRDTEF 568

RESULT 10
 K6P1_KLULA STANDARD; PRT; 992 AA.

AC 003215;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 6-phosphofructokinase alpha subunit (EC 2.7.1.11) (Phosphofructokinase 1) (Phosphohexokinase) (6PF-1-K alpha subunit).
 GN PFK1.
 OS Kluveromyces lactic (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=9331653; PubMed=8326866;
 RA Heinisch J.J., Kirchbach L., Liesen T., Vogelens K., Hollenberg C.P.;
 RT Molecular genetics of phosphofructokinase in the yeast Kluveromyces lacticus.";
 RL Mol. Microbiol. 8:559-570(1993).
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.
 CC -1- ENZYME REGULATION: Allosterically inhibited by ATP and activated by AMP and fructose 2,6-bisphosphate.
 CC -1- PATHWAY: Key control step of glycolysis.
 CC -1- SUBUNIT: Heterodimer of 4 alpha and 4 beta chains.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: Belongs to the phosphofructokinase family. Two domains subfamily.
 CC -----
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 CC -----
 CC EMBL: Z17315; CA78963.1; .
 CC DR PIR: S32902; S32902.
 CC DR HSSP: P00512; 3PFK.
 CC DR InterPro: IPR000023; Pfkuckinase.
 CC DR Pfam: PF00365; PFK; 2
 CC DR PRINTS: PR00476; PFERCKINASE.
 CC DR PRODOM: PD000707; Pfkuckinase; 2.
 CC DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 2.
 CC KW Kinase; Transferase; Glycolysis; Repeat; Allosteric enzyme.

SQ SEQUENCE 992 AA; 109336 MW; 724687850F2779 CRG4;
 Query Match 10.7%; Score 245.5; DB 1; Length 992;
 Best Local Similarity 23.8%; Pred. No. 5.1e-09;
 Matches 108; Conservative 74; Mismatches 165; Indels 107; Gaps 19;

QY 30 NKPKNVILTPGALPCINSLIGSLIEREIDSEIICRGCGYKGLLDSDYPTAV 89
 DB 181 SKKKKIAWTSIGSDSGQGNAAVAVVR--SIIYGCYVAVYBGBGVKGDYLRKMW 238
 QY 90 RKKAGVLFQFGSVYIGNSRVLTIVKDCVKGGLKEGD--PKRYAADQVKGVDILHT 147
 DB 239 KDVAQWLSR--GGTLIGTAR-----SKERREKGRQAQSNLIDGIDILVY 283
 QY 148 IGGDDTTAA-----ADLAFLARN-----YGLTVIGLPTKVDNDVPPIKOS 190
 DB 284 IGGDGSUTGADLFRSEWPSIVBELYKQKTEDEVALYOMLTIVGWGSDIDMDSGTST 343
 QY 191 IGAWTAEGAGRYEMVAVENNANPMLIVHEWGRNCWLT-----TAATQOEYKLLDRA 246
 DB 344 IGAYSLERICEMWDYIDATAKSHSAFVY-EVWGHCGLMLMGIALGADY----- 395
 QY 247 EMLPELGLTRSYEVAVPEPMALILEAKRLREVMKVCVNTIVSFGA- 298
 DB 396 -----IFIPERAAPEKQKQDELEKVCQRHSKGRNN--TVIARGL 436
 QY 299 --GVEAIVAEWQK-----QGVPRDAFHIKL--DAVNPQKPGQEPQMGIGAEKTV 348
 DB 437 DDQNPVTAE-QVNDVLEGLDPTKTLTIGHVQGGTAVAHDRMLAT--LQGVDAVAVATL 493
 QY 349 ----OKSGYAPASASNVDMKRLKSCADLAVECAFRESGVIGHDEDNQVRAIEFPR 404
 DB 494 NMPETSPILIGLENKILRMPLVES-----VLTQVAAIAEKDKAISLRDTEFIE 548
 QY 405 I-----KSGKPNIDTFWNSMLSEIQP 428
 DB 549 LYSNFMSTVNDGSQLPEADRLTAIVAGAP 582

RESULT 11

K6P1_CLOPE STANDARD; PRT; 319 AA.

AC Q8XNH2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase) (Phosphohexokinase).
 GN PFKA OR PFK OR CPO361.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / Type A.
 RX MEDLINE=21664373; PubMed=1192842;
 RA Shimizu T., Ohnani K., Hirakawa H., Oshima K., Yamashita A., Siba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater".;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.
 CC -1- PATHWAY: Key control step of glycolysis.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
 CC -----
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CC EMBL; AP003186; BAB0067.1; -

CC HANAP; MF_00339; -; 1.

DR InterPro; IPR000023; Pffruckinase.

DR Pfam; PF00365; PK; 1.

DR PRINTS; PR00476; PHRCKINASE.

DR PRODOM; PD000707; Pfpruckinase; 1.

DR PROSITE; PS00433; PHOSPHOFUCTOKINASE; FALSE NEG.

KW Kinase; transferase; Glycolysis; Complete proteome.

SQ SEQUENCE 319 AA; 3406 MW; 95DESCAFRA1IDF48 CRC64;

Query Match 10.6%; Score 242; DB 1; Length 319;

Best Local Similarity 25.9%; Pred. No. 2.1e-09;

Matches 103; Conservative 58; Mismatches 121; Indels 116; Gaps 18;

QY 33 KKVALLTAGLAPCLNSAIGSLIRYTEIDPSIIEICRGYKGLLGDSPYTAVERKK 92

DB 2 KKIIVLISGDAPEGMAALRAVTR--MALHHGLVGVGKGYAGLNGELFRVD--RKS 56

QY 93 AGVLAQRGGSVTGNRYKLTNVKDCVKRGLVKGSEDPQKAAADLVKD--GYDILHTIGSD 151

DB 57 VSEIINNGSTILRTAR--CLL--FKQEEVEKKA--QILKAYGEALVWIGSD 103

QY 152 DITFAADLAFLANNYGLTVIGLPTVNDVPIKQSGAMTAAGARFANVAAE- 210

DB 104 GSEFGAKLL-----SKLGVTAGLPGTIDNLSYTYTTFGPTD-----LNTVDA 149

QY 211 -----NNANPMLIVHEVGNRCGLTAATAGYERKLDRAWLELIGL/RESYEVHA 263

DB 150 INKLKDTSTHSRYSIV-EVGRNCGDLAL-----VAGIGAGAE-----A 188

QY 264 VFVEEMIDLEAKLE--VMDKVCNIFVSEGVAYAAE--MQAKGQVPRDAF 319

DB 189 IIVKMPDKDLIKTLLEGRTKTSI--IIVAGVGSEILKEIKESVTGISTRATIL 247

QY 320 GHILDAVNPQKWPGEOPAWIGAEKTLVOKSGYFARASASVNDKILKSCADLVECA 379

DB 248 GHID-----RGSPETDDIYLAIRMGAKVEVL 275

QY 380 FR-RESGVTGHDENGVLAIERPRKKGKPRNIDV 416

DB 276 LSGKTSKVIQ-----IKENRIFDMID 297

RESULT 12

K6PF_SALTY STANDARD; PRT; 320 AA.

AC QKAGLS;

DT 28-FEB-2003 (Rel. 41, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)

GN PFKA OR STM4062 OR STY3809 OR T3557.

OS Salmonella typhimurium, and

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_Taxid=602, 601;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=S.typhi; STRAIN=LT2 / SSGC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Portolillo S., Ali J., Dante M., Du P., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Gwral N., Mulvaney B., Ryan B., Sun H., Flores L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

RT "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2."

RL Nature 413:852-856(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=S.typhi; STRAIN=CT18;

RX MEDLINE=21534947; PubMed=11677608;

RA Churchill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M., Baker S., Basham D., Brooks K., Chillingworth T., Conerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Barrer J., Rellwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;

RT "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."

RL Nature 413:848-852(2001).

RN [3]

RP SEQUENCE FROM N.A.

RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;

RX MEDLINE=22513167; PubMed=1264504;

RA Deng W., Lion S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Birdand V., Kodoyanni V., Schwartz D.C., Blatter P.R.;

RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18."

RL J. Bacteriol. 185:2330-2337(2003).

CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.

CC -1- PATHWAY: Key control step of glycolysis.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: Belongs to the phosphofructokinase family.

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CC EMBL; AE008889; AAL22902.1; -

DR EMBL; AL627279; CAD9562.1; -

DR EMBL; AB016846; AAO71062.1; -

DR StyGene; SG7777; PfKA.

DR HAMAP; MF_00339; -; 1.

DR InterPro; IPR000023; Pfpruckinase.

DR Pfam; PF00365; PK; 1.

DR PRINTS; PR00476; PHRCKINASE.

DR PRODOM; PD000707; Pfpruckinase; 1.

DR PROSITE; PS00433; PHOSPHOFUCTOKINASE; 1.

KW Kinase; transferase; Glycolysis; Complete proteome.

SQ SEQUENCE 320 AA; 34915 MW; 68B0DDCF689F420 CRC64;

Query Match 10.5%; Score 240.5; DB 1; Length 320;

Best Local Similarity 24.8%; Pred. No. 2.7e-09;

Matches 102; Conservative 59; Mismatches 122; Indels 129; Gaps 18;

QY 33 KKVALLTAGLAPCLNSAIGSLIRYTEIDPSIIEICRGYKGL-----LIGDSPYTA 87

DB 3 KKIIVLISGDAPEGMAALRAVTR--MALHHGLVGVGKGYAGLNGELFRVD--RKS 56

QY 98 EVRKAGVLAQRGGSVTGNRYKLTNVKDCVKRGLVKGSEDPQKAAADLVKD--GYDILHT 147

DB 61 MINR-----GTFPLSAR--PFRVD-----ENTRAVAIENTLKRGIDALVY 100

QY 148 IGGDDTNAADLAFLANNYGLTVIGLPTVNDVPIKQSGAMTAAGARFANVAAE 207

DB 101 IGGDSYWKAKLL-----TEMGFPICIGLPGTIDNDIKGTDTTISYFALGTVVAIDRL 154

QY 208 VAENNANPMLIVHEVGNRCGLTAATAGYERKLDRAWLELIGL/RESYEVHA 265

DB 155 RDTSSSHORISIV-EVGRNCGDLTAATAGYERKLDRAWLELIGL/RESYEVHA 200

QY 266 VFVEEMIDLEAKLE--VMDKVCNIFVSEGVAYAAE--MQAKGQVPRDAF 310

DB 201 -----DLVAETKAGIKKKKHAIVATENKCDVDELAHFIEKTEGRETATVAGHIORG 254
 QY 311 GQWEPDPAFGHIKLDVAVNPGWPCGQPAOMIGAKTLVOKSGYAFASASVNDWMLIKS 370
 DB 255 GSPVEYD-----RILASMGVAV-----272
 QY 371 CADLAVE-----CAFRSGVIGHDENGVNLRATIEPRFKGKRPRIIDTW 417
 DB 273 -IDLHGHGRCVGIQNEQVHVD-----IDIAIENMK-----RPFK--SDW 312

RESULT 13
 K6P1_ECOLI
 ID K6P1_ECOLI STANDARD; PRT; 320 AA.
 AC P06936;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 28-FEB-2003 (Rel. 41, last sequence update)
 DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE 6-phosphofructokinase isozyme I (EC 2.7.1.11) (Phosphofructokinase-1)
 GN PFKA OR B3916 OR 25460 OR ECS4841 OR SF3994.
 OS Escherichia coli,
 OS Escherichia coli O157:H7, and
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 NCBI_TaxID=562, 83334, 623;
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli;
 RX MEDLINE=85203917; PubMed=3158524;
 RA Hellinga H.W., Evans P.R.;
 RT "Nucleotide sequence and high-level expression of the major
 RL Escherichia coli phosphofructokinase.";
 RL Eur. J. Biochem. 149:363-373(1985).
 RN
 RP REVISIONS, AND MUTAGENESIS.
 RC SPECIES=E.coli;
 RX MEDLINE=87229041; PubMed=2953977;
 RA Hellinga H.W., Evans P.R.;
 RT "Mutations in the active site of Escherichia coli
 RL phosphofructokinase.";
 RL Nature 327:437-439(1987).
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=93347969; PubMed=8346018;
 RA Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
 RT "Analysis of the Escherichia coli genome. III. DNA sequence of the
 RL region from 87.2 to 89.2 minutes.";
 RL Nucleic Acids Res. 21:3391-3398(1993).
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boulton A., Siao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimmlanta E.T., Potomousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7,";
 RL Nature 409:529-533(2001).
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi W., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo H., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12.";

RL DNA Res. 8:11-22(2001).
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=12384590;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Sun L., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao Y., Gao Y., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RL through comparison with genomes of Escherichia coli K12 and O157,";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RC SPECIES=E.coli;
 RX MEDLINE=89125622; PubMed=2975709;
 RA Shirkkhan Y., Evans P.R.;
 RT "Crystal structure of the complex of phosphofructokinase from
 RL Escherichia coli with its reaction products.";
 RL J. Mol. Biol. 204:973-994(1988).
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.
 CC -1- ENZYME REGULATION: SUBJECT TO ALLOSTERIC ACTIVATION BY ADP AND OTHER DIPHOSPHONICLOSIDES, AND INHIBITION BY PHOSPHOMOLYPHATE.
 CC -1- PATHWAY: Key control step of glycolysis.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: E.COLI HAS TWO 6-PHOSPHOFRUCTOKINASES ENZYMES.
 CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL, X02519; CAA26356.1; -
 DR EMBL, L19201; AAB03048.1; -
 DR EMBL, AE000466; AAC76898.1; -
 DR EMBL, AE005622; AAG59109.1; -
 DR EMBL, AP002567; BAB38264.1; -
 DR EMBL, AE015406; AAN45428.1; ALT_INIT.
 DR PIR, A86081; A86081.
 DR PIR, A98234; A98234.
 DR PIR, G65197; KIECPA.
 DR PDB, 1PFK; 15-OCT-92.
 DR SWISS-2DPAGE; P06998; COLI.
 DR EC02DBASE; F035.8; 6TH EDITION.
 DR Ecogene; EG106599; PFKA.
 DR HAMAP; MF_003399; -; 1.
 DR InterPro; IPR000023; Pfrfructinase.
 DR Pfam; PF00365; PFK_1.
 DR PRINTS; PR00476; PFRFRCTINASE.
 DR ProDom; PD000707; Pfrfructinase. 1.
 DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE. 1.
 KW Kinase, Transferase, Glycolysis, 3D-structure, Allosteric enzyme;
 KW Complete proteome.
 FT ACT_SITE 128
 FT MUTAGEN 128 128
 FT MUTAGEN 172 172
 FT
 FT CONFLICT 74 74 P -> C (IN REF. 1).
 FT CONFLICT 103 104 GD -> DG (IN REF. 1).
 FT CONFLICT 163 163 R -> P (IN REF. 1).
 FT STRAND 317 319 KKL -> EKM (IN REF. 1).
 FT TURN 4 9
 FT TURN 15 16
 FT HELIX 17 30
 FT TURN 31 32

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FT STRAND 34 38
FT TURN 40 40
FT HELIX 41 46
FT TURN 47 48
FT STRAND 50 53
FT HELIX 56 58
FT TURN 59 60
FT TURN 62 63
FT TURN 68 69
FT HELIX 75 78
FT HELIX 80 92
FT TURN 93 94
FT STRAND 97 102
FT HELIX 104 115
FT TURN 116 117
FT STRAND 120 125
FT TURN 127 128
FT TURN 132 133
FT STRAND 138 138
FT TURN 139 139
FT HELIX 140 161
FT TURN 162 162
FT STRAND 164 169
FT TURN 172 173
FT HELIX 176 184
FT TURN 185 186
FT STRAND 189 191
FT TURN 193 194
FT HELIX 199 211
FT TURN 212 213
FT STRAND 217 222
FT HELIX 228 239
FT STRAND 243 247
FT HELIX 249 253
FT TURN 259 278
FT STRAND 279 289
FT STRAND 283 288
FT TURN 289 290
FT STRAND 291 296
FT HELIX 297 303
FT HELIX 310 320
SQ SEQUENCE 320 AA; 34842 MW; D03D79F6A5536A41 CRC64;

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Query Match 10.4%; Score 238.5; DB 1; Length 320;
Best Local Similarity 24.9%; Pred. No. 3.7e-09;
Matches 100; Conservative 65; Mismatches 132; Indels 105; Gaps 18;

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QY 33 KKVAILTAGLAPCLNSAIGSLIERYTEIDPSIEITCTRGYKGL-----LGGSPYTA 87
DB 3 KXIGVLTGSGDAPFKNAAIRGVVR--SALTGELFVWGIDYGLYEDRMVQLDRYSVSD 60
QY 88 EVRKKAAGVLRQFGSGVINSRVKLVNVDQVKGIVGEGEDPOKVAADQVKGVDILHT 147
DB 61 MINR-----GGTFLLSAR--PREFD-----ENIRAVAIENLKKRGIDALVY 100
QY 148 IGGDDTNTAAADLAAFLARNNYGLTVIGLPKTVNDVFPKISGIGAMTAAEQARYPNV 207
DB 101 IGGDGSYMGAKRL-----TEMGFPICIGLPGIINDIKGTYYTIGFFALSTVVEALDRL 154
QY 208 VAENNANRMLIVHEVMGRCNCWTLAATNOGRKLLDAEW--LPDELGTSESYEVNAVF 265
DB 155 RDTSSSHRISIV--EVMGRYCGDLTLAA-----IAGGCEVAVVEVFEFSRD-----L 202
QY 266 VPEMAIDLEAEAKR-----LREVMKVDVCNIFVSEGAIVE--AIYAEQAKQEQEVRD 317
DB 203 VNEIRAGI--AKGKKAIVAITHEMCDVDDELAFHEIKETGRTFATVLGHIGRGSPYVD 261
QY 318 AFGRHKDAVNPGRKPGSQPACMTAETIVOKSYFPAASASVNDMRLKSCADLAIVE 377
DB 262 RI-----LASRMGAVALDILLAYGGR----- 283
QY 378 CAFRESGVIGHEDNGVNLRAIEPPRIKGGKPFNIDWTEN 419

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DB 284 CAGIQNEQLVHED-----ITDAIENMK-----RPFK--GDWLD 314

RESULT 14
K6PF YERP ID STANDARD; PRT; 327 AA.
AC Q82J6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
DE (Phosphohexokinase)
GN PRKX OR YPO0078 OR Y0059.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_Taxid=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11386360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarrega A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Slimmons M., Skelton J., Stevens K., Whitehead S., Barrall B.G.,
RA "Genome sequence of Yersinia pestis, the causative agent of plague,"
RA Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G., III, Bourin A., Mayhew G.F., Lise P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.B., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RU J. Bacteriol. 184:4601-4611(2002).
CC -1- CATALYTIC ACTIVITY: ADP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -1- PATHWAY: Key control step of glycolysis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
CC
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CC
DR EMBL: AJ14141; CAC88944.1; -
DR EMBL: AB013607; AAM83654.1; -
DR PIR: AF0010; AF0010.
DR HAMAP: MF 00339; -.
DR InterPro: IPR000023; Pffructkinase.
DR Pfam: PF00365; PFK.
DR PRINTS: PR00476; PFRCTKINASE.
DR ProDom: PD000707; Pfructkinase.
DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
KW Kinase; Transferase; Glycolysis; Complete proteome.
SQ SEQUENCE 327 AA; 35394 MW; 1D54B3BAED0E430D CRC64;

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Query Match 10.3%; Score 234.5; DB 1; Length 327;
Best Local Similarity 27.2%; Pred. No. 7.1e-09;
Matches 84; Conservative 50; Mismatches 102; Indels 73; Gaps 13;
QY 33 KKVAILTAGLAPCLNSAIGSLIERYTEIDPSIEITCTRGYKGLGG-----DSYPTA 87

```


DB 3 KGIAGLVTSAGDADGNNAAIRGVVR--AALSAGLDVFGIEDYGLYENRKKKIDRYSVD 60
 QY 88 EVKKKAGVLRFGGSVYGNRKYLTNKKCCYKGLYKGGEDPO--KYAADQLYKGVLDL 145
 DB 61 MIRN-----GGTFIAGSAR-----PPEFRDPYEVKVALNMRERIGDGL 98
 QY 146 HTTGDDDTTAAADIAFLARNNYGLTVIGLPTVDNDVFPPIKOSIGAWTAAGARFYM 205
 DB 99 VVIQGDG-SYAGADLLEZ---KEGGHCVGLPGTINDVAGTDYTTIGFTALLETVEALD 153
 QY 206 NVAAENNANRMLIVHEWGRNCGWLTAACTAOERYKLDRAEW--LPELGLTESYEVAH 263
 DB 154 RLDDTSSHQRIISIV-EVMGRYCGDLTLAA--IAGCEFTALPEVEFKSD----- 201
 QY 264 VFPEPAIDLEAAK-----RLREVDKXDCVNIIVSEGAQVE---AIYAEMQ 308
 DB 202 -----DLVAETIKGIAKKGKHAIVALTETKDDIDSLAKYLEKERTGRTGVIGHIO 253
 QY 309 AKGOEVPD 317
 DB 254 RGAPVAYD 262

RESULT 15
 K6PF_BACMC STANDARD; PRT; 322 AA.

AC 059214;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
 DE (Phosphohexokinase).
 GN PFKA OR PFK.
 OS *Bacillus macquariensis*.
 OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
 NCBI_TaxID=1468;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23464;
 RX MEDLINE=96257193; PubMed=8675031;
 RA Rouwendal G.J.A., Zwiers L.H., Wolbert E.J.H., Springer J.,
 RA Moolbroek H., Huizing H.J.,
 RA "Cloning, sequence and expression in *Escherichia coli* of the gene
 RT encoding phosphofructokinase from *Bacillus macquariensis*,"
 RL Gene 171:59-63(1996).
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
 fructose 1,6-bisphosphate.
 CC -1- PATHWAY: Key control step of glycolysis.
 CC -1- SUBUNIT: Homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: X76484; CAA54022.1; -.
 DR PIR: S39248; S39248.
 DR HSSP: P00512; 3PFK. 1.
 DR HAMAP: MF_00339; -; 1.
 DR InterPro: IPR000023; Pfkfructinase.
 DR Pfam: PF00365; PFK. 1.
 DR PRINTS: PR00476; PFRCTKINASE.
 DR ProDom: PD000707; Pfkfructinase; 1.
 DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
 KW Kinase, Transferase, Glycolysis.
 SQ SEQUENCE 322 AA; 34648 MW; 2C156F42669EC46C CRC64;

Query Match 10.2%; Score 233.5; DB 1; Length 322;

Best local similarity 25.2%; Pred. No. 8 le-09;
 Matches 101; Conservative 68; Mismatches 141; Indels 91; Gaps 17;
 QY 33 KVAAILTAGLAPCLINSAIGLIBERYTEIDPISIEIICRGGYKGLLDGSPYPAVERK 92
 DB 4 KKIAYITSGDSQGNMAAVAVVR--SGLFYGLFVYGIQRYGILLNDIIF--SMDLRSV 59
 QY 93 AGVLQRFQGSVYGNRKYLTNKKCCYKGLYKGGEDPOKYAADQLYKGVLDLHTIGSD 152
 DB 60 GDILQF-GFTVLIQSAR-----CKEFTPEG---QKQADILRKRGIDGLVVIQSDG 106
 QY 153 TTTAAADIAFLARNNYGLTVIGLPTVDNDVFPPIKOSIGAWTAAGARFYMNVAAENH 212
 DB 107 SYHGNK-----SKLGINTMALPGTINDSDSYDPTTGFTSIVSVADANLKLRTMS 160
 QY 213 ANPRMLIVHEWGRNCGWLTAACTAOERYKLDRAEWLPELGLTRSYEVAHVFPEPAID 272
 DB 161 SHRRSSIV-EVMGRYCGDLTLA--YAGLASGAS-----TIIVEVPPD 199
 QY 273 LEAAKRLRE--VMDKXDCVNIIVSEGAQVEAIYAMQAKGOEVPDRDAGHKLDVAVNG 330
 DB 200 MDEIARMKQNPFAHGRKHSI-VVAEGAG-----NGENYAK----- 234
 QY 331 KMFGEQFQMTIGAEKTL--VQKSGYFARASAVNDNKLKSCADLAVECAFRES-- 384
 DB 235 -----QLVERCETLEPRVTVLGHIOGGTPTPADRLASRLDDPAVRMLIAGBSAVA 286
 QY 385 -GVIGHDENKNVLAIEPPRIKGGKPPNIDDMNSHISE 424
 DB 287 CGII-----SNELVITDID-KVYNSKKEPMELYELAAHLSQ 322

Search completed: January 29, 2004, 14:37:01
 Job time : 18 secs

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OM protein - protein search, using sw model

Run on: January 29, 2004, 14:30:22 ; Search time 40 Seconds
(without alignments)
2819.225 Million cell updates/sec

Title: US-09-941-947A-2

Perfect score: 2284
Sequence: 1 DVVTMPHYLTADIRCHWPF.....FNSMLSEIGQKGVKVEVSH 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMEL_23.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_proteus.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriophage.*
17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1453	63.6	410	5 Q9NGP6	Q9NGP6 mastigamoeb
2	1302	57.0	404	16 Q92NK9	Q92NK9 rhizobium m
3	1292.5	56.6	514	16 Q8UDL0	Q8UDL0 agrobacteri
4	305	13.4	346	2 Q9KH71	Q9KH71 dictyoglomu
5	282	12.3	488	10 Q9FUT5	Q9FUT5 arabisdopsis
6	281.5	12.3	485	10 Q9C5U7	Q9C5U7 arabisdopsis
7	278	12.2	366	16 Q8XU57	Q8XU57 clostridium
8	274.5	12.0	341	2 Q9AGC0	Q9AGC0 amycolatops
9	270	11.8	448	16 Q94AA4	Q94AA4 arabisdopsis
10	266	11.6	489	10 Q94AA4	Q94AA4 arabisdopsis
11	263.5	11.5	436	5 Q97651	Q97651 entamoeba h
12	260.5	11.4	586	10 Q94J12	Q94J12 cryza sativ
13	260.5	11.4	775	10 Q94J12	Q94J12 cryza sativ
14	260	11.4	382	5 Q24812	Q24812 entamoeba h
15	257.5	11.3	500	10 Q9ST07	Q9ST07 arabisdopsis
16	253	11.1	473	10 Q817L4	Q817L4 arabisdopsis

17	252	11.0	459	2 Q8VU09	Q8VU09 amycolatops
18	252	11.0	487	5 Q15648	Q15648 trypanosoma
19	251	11.0	473	10 Q9M0F9	Q9M0F9 arabisdopsis
20	250	10.9	426	5 Q61068	Q61068 trichomonas
21	248.5	10.9	437	5 Q27705	Q27705 naegleria f
22	245	10.7	324	2 Q8GNC1	Q8GNC1 haemophilus
23	245	10.7	431	16 Q8EXU6	Q8EXU6 leptospira
24	244.5	10.7	486	5 Q9BIC6	Q9BIC6 leishmania
25	243	10.6	462	10 Q9M076	Q9M076 arabisdopsis
26	240.5	10.5	352	16 Q8FBD0	Q8FBD0 escherichia
27	240	10.5	337	1 Q57694	Q57694 thermoprote
28	239	10.5	462	10 Q8LA55	Q8LA55 arabisdopsis
29	235	10.3	390	16 Q8KRS2	Q8KRS2 chlorobium
30	234	10.2	530	10 Q9FKG3	Q9FKG3 arabisdopsis
31	232	10.2	461	16 Q83146	Q83146 treponema p
32	226.5	9.9	444	10 Q9F1K0	Q9F1K0 treponema p
33	223.5	9.8	921	5 Q8SSA3	Q8SSA3 encephalito
34	222.5	9.7	361	2 Q9S479	Q9S479 myxococcus
35	221	9.7	335	16 Q8DQ85	Q8DQ85 streptococc
36	221	9.7	490	5 Q8WPR2	Q8WPR2 trypanoplas
37	220	9.6	573	16 Q83553	Q83553 treponema p
38	218	9.5	750	4 Q96160	Q96160 homo sapien
39	217.5	9.5	320	16 Q8DCY1	Q8DCY1 vibrio vuln
40	217.5	9.5	537	10 Q8VYN6	Q8VYN6 arabisdopsis
41	216	9.5	784	11 Q8C605	Q8C605 mus musculu
42	213.5	9.3	775	3 Q9H3Z0	Q9H3Z0 aspergillus
43	212.5	9.3	337	16 Q8DIX6	Q8DIX6 streptococc
44	212.5	9.3	549	2 Q9FAE8	Q9FAE8 porphyromon
45	212	9.3	784	11 Q8C516	Q8C516 mus musculu

ALIGNMENTS

RESULT 1	Q9NGP6	PRELIMINARY;	PRT;	410 AA.
ID	Q9NGP6			
AC	Q9NGP6			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DS	PPI-phosphotransferase (EC 2.7.1.11).			
GN	PPIase.			
OS	Mastigamoeba balamuthi (Phreatamoeba balamuthi).			
OC	Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.			
OX	NCBI_TaxID=108607;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Lee J.A., Moore D., Sensen C.W., Gaasterland T., Muller M.,			
RT	"cDNA clones (expressed sequence tags) from the free-living			
RT	amitochondriate amoeboid flagellate Mastigamoeba balamuthi."			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF246209; AAF70463.1; -			
DR	InterPro: IPR000023; PPIase_kinase.			
DR	Pfam: PF00365; PPIase_kinase.			
DR	PRINTS; PR00476; PPIase_kinase.			
DR	ProDom; PD000707; PPIase_kinase; 1.			
KW	Kinase; Transferase.			
SO	SEQUENCE 410 AA; 44200 MW; CD362D1D2D41A0D0 CRC64;			
Query Match	63.6%; Score 1453; DB 5; Length 410;			
Best Local Similarity	67.2%; Pred. No. 2.8e-99;			
Matches 272; Conservative 55; Mismatches 78; Indels 0; Gaps 0;				
Qy	33 KKVAILTAGGLAPCLNSAIGSLIERETEDPSIEIICRYGKYGKLLGDSYPYTAVERKK 92			
Db	3 KTVAILTAGGLAPCLNSAIGSLIERETEDPSIEIICRYGKYGKLLGDSYPYTAVERKK 92			
Qy	93 AGTLQRFSGSVIGNSRYKLTNVDCYKRGIVYEGSDPQKRAAPLVKDDVLIATIGGD 152			
Db	63 AAVLQTFSGSVIGNSRYKLTNVDCYKRGIVYEGSDPQKRAAPLVKDDVLIATIGGD 122			
Qy	153 TTTAAADLAFLAFLRNRYGLTVIGLPTVNDVDFPIKQSLGATPAAGAGARYFNNVVAENN 212			

Db	123	TNTAAADLAAVYUAAHGYTLTRVIGLPTINDIVPRLQSLGANTAAEQSLFFQVAAEQT	182
Qy	213	ANPRMLIVHEVMGRNGMTLTATQOERYKLIDRAEHLPELGITRESEVTAAYVEPAKD	272
Db	183	ANPRVLTVEHWKRSQGYLTPQADRYRQLNHRFPDELGHTREYDIIAAVVEPTID	242
Qy	273	LEABAKELREVMKVDVCNIVFSEGAQVBAIVAEHQAOGEVPRDQHIKLDVANGXW	332
Db	243	LKBAARLTRVMRVCQVNIPLSEGGINDIVIAEMTATGCTVPRDPFGHVIDIINGAW	302
Qy	333	FGSQPQMTIAEKTIVQKSGYFPABASAVDDMTIKSCALAYECAFRRSGYIGDED	392
Db	303	FGQFQPGMWADKYLVDQKSGYFSRSLPAAAEULRIIKGVMDLAQDCLRGAAGLIGDSE	362
Qy	393	NGAVLALIEPRRKGGKFPNIDTDMFNSMLSTIGOPKGGKTEVSH	437
Db	363	RNGVLRLIEFERVKGAAPNIDHPWTHLNETIGPDKAKSVAH	407

RESULT 2	PRELIMINARY:	PRT:	404 AA.
092NK9			
AC	092NK9		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Probable leucylphosphatase--fructose 6-phosphate 1-phosphotransferase		
DE	protein (EC 2.7.1.90).		
GN	PFK OR R02190 OR SMC01862.		
OS	Rhizobium meliloti (Sinorhizobium meliloti).		
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;		
OC	Rhizobiaceae; Sinorhizobium.		
OX	NCBI_TaxId=382;		
RP	[1]		
RF	SEQUENCES FROM N.A.		
RC	STRAIN=1021;		
RA	MEDLINE=21396507; PubMed=11481430;		
RA	Capeia D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J		
RA	Boisard P., Becker A., Boutry M., Cadieu E., Dreno S., Gloux S.		
RA	Godrie T., Goffeau A., Kahn D., Kiss E., Lelaire V., Masny D.,		
RA	Renal T., Portecaille D., Puhler A., Purnelle B., Ransperger U.,		
RA	Richard C., Theault P., Vanderbol M., Weidner S., Gallbert F.;		
RT	"Analysis of the chromosome sequence of the legume symbiont		
RT	Sinorhizobium meliloti strain 1021."		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).		
DR	EMBL: AL591789; CAC46765.1;		
DR	InterPro: IPR000023; PfkTnckinase.		
DR	Pfam: PF00365; PFK, 1.		
DR	PRINTS: PR00476; PHPCKTINASE.		
DR	Prodom: ED000707; PpfTnckinase; 1.		
DR	Transferase; Complete proteome.		
SD	SEQUENCE 404 AA; 43712 MW; 1F65ECD966A13D5 CRC64;		

	Query Match	57.0%;	Score 1302;	DS 16	Length 404;
	Best Local Similarity	62.3%;	Pred. No. 4.2e-88;		
	Matches 246;	Conservative 59;	Mismatches 90;	Indels 0;	Gaps 0
QY	KKVAITTAGAGLPPCNSAIGSLERKYEETIDPSIRIIICRGSGYGLLGGSPYTALEVRKK	92			
Db	KKVAMTAKAGLAPCGLSSAVGSLERYETIDLADYELVATRSYGQGLLADLRIRTPPMREK	63			
QY	AGLQRFSGSGVSGSRVRLTWMYKDCYKRGVKEEEDPPKQAAAOIKMGDGIITLTGGD	152			
Db	AYLHRRGSGPLGNSRVLTMTADCYKRGVKEEENPLRAARLRLASDGLSILTIITGGD	123			
QY	TTTTAAADLAALFLARNYGLTIVIGLPTVNDVYFIIKSLGAWTAALGAGAFYEMTVAAENK	212			
Db	TTTTAADLAAITAGNAGTDLTVVGPEKTVNDNVYIRKTLGAMTAALGAFYFDHNSNEOS	183			
QY	ANPRMLIVHEVMGRNCGMLTAATAOERYKLLDRAEMLPELGLTRSESYAHAAVFPVEMALD	272			
Db	AAERLTIVAEVWGRRCGMILTAATAAYTHLAGNKEVYDGEEMMAKQJKNIDGLYPEMAFD	243			

Qy 273 LEAEARLRREMDKXVCVNI FVSESGAEVATVEMQAGQSEPPRAFHITLIDLVNGM 332
Db 244 LEAEARLRREMDRAGFVTILFVSESGCIDALVABREBAAGETVKGDAFHVAVIDITVNGM 303
Qy 333 FGGSGPQMIGABKTLVQKSGYFAPRASAANVDMRLIKSCALVAYCARRESGVTGHED 339
Db 304 FSGQFPALLGABRSWQVQSGYFAKSAHPANVDDRLIQGMVDLVAYSLAKIKSGVTHED 365
Qy 393 NGNVYALIEPRRIKGGKXPNIDTDFNMSLSEIQ 427
Db 364 QGGRLNTIEPRRIKGGKHEVDTSAKFAFGEMDVVQ 398

RESULT 3		
C8UDL0	PRT;	514 AA.
ID Q8UDL0	PRELIMINARY;	
AC Q8UDL0		
DT 01-JUN-2002	(TREMBLE)rel. 21, Created)	
DT 01-JUN-2002	(TREMBLE)rel. 21, Last sequence update)	
DT 01-MAR-2003	(TREMBLE)rel. 23, Last annotation update)	
DE PYP Phosphatase--fructose-6-phosphate 1-phosphotransferase.		
GN PYP OR ATU2115 OR AGR C 3836.		
OS Acrobacterium tumefaciens (strain CS8 / ATCC 33970).		
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales		
OC Rhizobiaceae; Rhizobium.		
OX NCBI_Taxid=176299;		
NN [1]		

RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monke D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
 RA Chen Y., Paulsen I.F., Eichen J.K., Katz P.D., Bovee D. Sr.,
 RA Chapman P., Glendinning T., Deatherage G., Giller W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-Y., McClelland E., Palmeri A.,
 RA Raymond C., Rouse G., Saenphithachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tiao L., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Meister E.W.;
 RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*
 RT C58."
 RL Science 294:2317-2323(2001).
 RN 12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Houmlo B., Goldman B.S., Cao Y., Askenazi M., Halling G., Mullin L.,
 RA Houmlo K., Gordon J., Vaudin M., Iatchouk O., Epp A., Liu F.,
 RA Molian C., Allinger M., Doughty D., Scott C., Lappas C., Marxz B.,
 RA Flanagan C., Crowell C., Gureson J., Lomo C., Sear C., Strub G.,
 RA Cleto C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT *Agrobacterium tumefaciens* C58".
 RL Science 294:2323-2328(2001).
 RL EMBL: AEO09161; AAL43105.1; ALT_INTT.
 DR EMBL: AEO08127; AAK87863.1; -
 DR InterPro: IPR000023, Pfam: pfam0355, Pfk_1.
 DR Pfam: pfam0355, Pfk_1.
 DR PRINTS: PR004766; PflRCKTNASE.
 DR PRODOM: PD000707, PflRCKTNASE, 1.
 DR TRANSFERASE; Complete proteome.
 QM SEQUENCE 514 AA; 55841 MW; B92DFT7E39F0E0AD CRC64;

Query Match	56.68	Score	1392.5	DB	16	Length	514
Best Local Similarity	57.98	Pred. No.	3.1e-87				
Matches	246	Conservative	71	Mismatches	101	Indels	7
						Gaps	2
OY	8	HLRADI----	RFGHEFLNFTLTANKPKKVAILLTGGALAPCLNSAIGSLIERYTEIDP				63
DB	89	HLHAAVASICTCLMWYAK--	RDAAWAKKQAVALLTGGALAPCLSSAAGGLIERISDIAF				145
OY	64	SIILITCRGGKYLHLLDSYPTVAEYKKKGVORFGGVSIGNSRVLTWVKDCVKEGLV					123

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146 EIDIIATSGVGLIGERIEITKMKRAHLIRHYGSPIGNSRVKLTNNADCAKGLV 205
124 KEGEDPOKVAADOLVKQGVDIHTITIGDDTNTAAADLAFLARNYGLTVGLPKTYND 183
206 KEGNDPLVAABERLAADGITIHTITIGDDTNTAAADLAAYIGANGYDLTVGLPKTYND 265
184 VFPIKOSIGANTTAABOGARFYMTVAENANPRLIYHEWGNRCGMILTAATQERYKL 243
266 VVPIKOSIGANTTAABOGAFAFDNNSNEQSAKPFVHEWGNRCGMILTAATQERYKL 325
244 DRAEMPELIGLTSREYVHAFVEMAIIDLBAKARLREVMKXDVCNIFVSEBAGYEA 303
326 RQNDYVEGLMNTOMKINDIGIYDPMADTIEABERLKEVMDKGYVTLFVSEBAGYEA 385
304 VAENQAGQEVPRDAFGHILKLDVNPGRKGEQAFOMIGAKTLVOKSGYFARASAVND 363
386 VAERBAAGAVKRDAPFGVKIDTINVGMFQKOPAGLIGERSWVOKGYFARASAVND 445
364 DMRLIXCADLAVCAFRBESGVIGHEDNGNVRAIEFPRIKGRFPNIDTMFNSML 423
446 DLRLIQGVNDLAVESALNKVSGVGHEDDQNGKLRTEFPRIKGRKFFLSAKWTEYME 505
QY 424 EIGQP 428
Db 506 HVGQP 510

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RESULT 4

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Q9KH71 PRELIMINARY; PRT; 346 AA.
ID Q9KH71;
AC Q9KH71;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Pfl-dependent phosphofructokinase.
GN PFP.
OS Dictyoglomus thermophilum.
OC Bacteria; Dictyoglomi; Dictyoglomales; Dictyoglomaceae; Dictyoglomus.
OX NCBI_TaxID=14;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RL46 B.1;
RX MEDLINE=20372656; PubMed=10913106;
RA Ding Y.-H.R., Ronimus R.S., Morgan H.W.;
RT "sequencing, cloning, and high-level expression of the pfp gene,
RT encoding a pfp-dependent phosphofructokinase from the extremely
RT thermophilic eubacterium Dictyoglomus thermophilum."
RL J. Bacteriol. 182:4661-4666 (2000).
DR EMBL; AF268276; AAF80100.1; -.
DR HSSP; P06998; 2PFX.
DR InterPro; IPR000023; Pfrfructinase.
DR Pfam; PF00365; PFK.1
DR PRINTS; PR00476; PFRCTKINASE.
DR ProDom; PD000707; Pfrfructinase; 1.
KW Kinase.
SQ SEQUENCE 346 AA; 37448 MW; 50C03B64BA7927F1 CRC64;

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Query Match 13.4%; Score 305; DB 2; Length 346;
Best Local Similarity 27.5%; Pred. No. 2, 2e-14;
Matches 107; Conservative 73; Mismatches 155; Indels 54; Gaps 15;
QY 34 KVALITAGLAPCLNSAIGSLIRYETIDPSIEIICRYGKYKLLIGDSYPTVAEYKKA 93
Db 5 RIVGLTGGGDCPGLNPAIRGIYMR--ALDYGVDEVIIGLKYGMAGLLKADTMPISLEVED- 61
QY 94 GVLQRRGSGVIGNSRVKLTNVNDCVKGGLYKGEDEPOKVAADOLVKQGVDIHTITIGDDT 153
Db 62 --ILBGGIGLSSR---TNP-----FKGEEDVQK--CVENFKLDLADALAGGSJT 107
QY 154 NTAADLAALFARNNYGLTVIGLPTVNDVFPPIKOSIGANTTAABOGARFYMTVAENANA 213
Db 108 LSVASXK-----SKGLPMIVGPKTIDKLBETDVTIGPDVAVEVVVAIKRLDTAS 161

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QY 214 NPRLIYHEWGNRCGMILTAATQERYKLDRABWLPFLGLTSREYVHAFVEMAIIDL 273
Db 162 HAAVIV-ELMGHAGML-----YGLAGADY-----ILIPVEPNL 200
QY 274 EAAKRLREVMK-VDCNIFVSEBAGYEAIVAEOMAKQGEVPRDAFGHILKLDVNFQK 332
Db 201 EDLYNRIKLYAGRNHAAVAVLAIEVQLPEFTYO---KQEGNVDAFGHILRGV--GNV 255
QY 333 FGEOPOMIGAKTLVOKSGYFARASAVNDMLIKSCADLAVECAFRESGVIGHED 392
Db 256 LAELIQKGLTEFRAYILS-HLQGGSPSTRDKIMELLQKAVDLVHBSKSLF--VAV 312
QY 393 NQNVLAIEFPRIKGRFPNIDTMFNSM 421
Db 313 KQNELVPDITLIE-GTKNVDPAFYESV 340

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RESULT 5

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Q9FJ05 PRELIMINARY; PRT; 488 AA.
ID Q9FJ05;
AC Q9FJ05;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Pyrophosphate-dependent phosphofructo-1-kinase-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Sequence features of the regions of 1,367,185 bp covered by 19
RT physically assigned P1 and TAC clones."
RL DNA Res. 5:203-216 (1998).
DR EMBL; AB013392; BAB09881.1; -.
DR HSSP; P00512; 3PFX.
DR InterPro; IPR000023; Pfrfructinase.
DR Pfam; PF00365; PFK.1
DR PRINTS; PR00476; PFRCTKINASE.
DR ProDom; PD000707; Pfrfructinase; 1.
KW Kinase.
SQ SEQUENCE 488 AA; 53781 MW; ABA526AED9213B17 CRC64;

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Query Match 12.3%; Score 282; DB 10; Length 488;
Best Local Similarity 26.8%; Pred. No. 1, 9e-12;
Matches 112; Conservative 60; Mismatches 156; Indels 86; Gaps 18;
QY 37 ILTAGLAPCLNSAIGSL-----IERYTEIDPSIEIICRYGKYKLLIGDSYPTVA 87
Db 96 IYTCGGLCGANTVIREVSSLSYKVGKRLIGDVSL-----CGYGFYAKNTIPLMS 149
QY 88 EYKKAAGLQRRGSGVIGNSRVKLTNVNDCVKGGLYKGEDEPOKVAADOLVKQGVDIHT 147
Db 150 KV--VNDIHRGGGTLITSR-----GQHTYTK--VSTIQRGNGYVT 189
QY 148 IGGDDTNTAAADLAFLARNYGLTVIGLPTVNDVFPPIKOSIGANTTAABOGARFY--M 205
Db 190 IGGDDTQGASVTFEIRRLRLKAVVGIPTINDIDVIDKSPGPDVAVEBAQAALINA 249
QY 206 NVVANNANPRLIYHEWGNRCGMILTAATQERYKLDRABWLPFLGLTSREYVHAF 265
Db 250 HVEAESNNGIGLV--KLMGYSGYIA-----WYATLASRDVDC 288
QY 266 VPEVAIDLEAFA-----KTLREVMKVDVCNIFVSEBAGYEAIVAEOMAKQGEVPRDA 318
Db 289 IPESFYLRGGGLPFLIERLRKHGHV-----IYLAGAGQDLAKMSMS-----TPDA 340

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QY 319 FGHKIDAVNPGKMFGEQFAQMI GAETLVQ---KSGTPARASASVNDMLIKSCADL 374
 DB 341 SGRKLLKDV---GLMISQSIKHDFKRNKMYNLTXYIDPTWIRAPSVASDNVYCTLLAQSG 398
 QY 375 AVACAFRRREGVGHDED--NENVLRAIEPRRIKGGKPPNIDD--WFNSMLSEIQP 428
 DB 399 AVHGA---AGTYGYSGLVNGR-QTYIPRYRITETQNNVITDRMKAR-LLSTNQP 451

RESULT 6

Q9C5J7 PRELIMINARY; PRT; 485 AA.

ID Q9C5J7
 AC Q9C5J7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative pyrophosphate-dependent phosphofructo-1-kinase.
 GN MK19.8/AT5G56630.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.D., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shimizu P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RT "Full length cDNA of gene MK19.8/AT5G56630 (GI:10176767).";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RA
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M.,
 RA Quach H.D., Tang C., Toriumi M., Yu G., Bowser L., Carninci P.,
 RA Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Kim C., Koeesema E., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shimizu P., Southwick A., Tracy S.E.,
 RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene MK19.8/AT5G56630 (GI:10176767).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RA
 RN [3]
 RP EMBL; AF360207; AK25917.1;
 DR EMBL; AY040055; AA64113.1;
 DR HSSP; P00512; 3PK;
 DR InterPro; IPR000023; Pfprckinase.
 DR Pfam; PF00365; PFK; 1.
 DR PRINTS; PR00476; PHPRCKINASE.
 DR PRODOM; PD000707; Pfprckinase; 1.
 DR KINASE; Complete proteome.
 SQ SEQUENCE 485 AA; 53482 MM; 6P0C6CF43BA7B5 CRC64;

Query Match 12.3%; Score 281.5; DB 10; Length 485;
 Best Local Similarity 26.7%; Pred. No. 2e-12;
 Matches 109; Conservative 61; Mismatches 166; Indels 73; Gaps 16;

QY 37 ILTAGLAPCNSAIGSLERTETDPSIEIICRYGKGLLGSYPYTAVERKKAQVL 96
 DB 96 IYTCGLCGALNTVIREVSSLSYMGVRRILGIDGIRGFYAKRTIPLNSRY--VNDI 152
 QY 97 QRFGEVINSRVLKTNVDCVKGIVKEGDEPKVAADQVLKDVILHTIGGGDTITA 156
 DB 153 HRRGGTITGSR-----GHDITNKL-VDSIDRGINQVYIIGGGGTORG 195
 QY 157 AADLAFLAARNYGLTVIGLPTVNDVFPFKISGARTAAEGKRYF--NAVVAENAN 214
 DB 156 ASVIEEIRRLKVAVVGIIPTITNDIPVIDISFGFTVAVEAQRALNAHVEAESNEN 255

QY 215 PMLIVHWGRNGMILTAAQAEYRLDLRAEWLPELGLTRESYEVHAFVPEMAIDLE 274
 DB 256 GIGFV--XLMGRYSGLY-----MYATIASADVDCCLIPSPFYLE 294
 QY 275 AEA-----RLEPMVKDCVNI FVSEAGVAEIVAMOKQGEVPRDAFGHKIDAV 327
 DB 295 GEGGLFETIERLKHGHMV---IYLAEGAGQDLMCKSNES---TMDASGNKLLKDV 346
 QY 328 NPGKWFGEQFAQMI GAETLVQ---KSGTPARASASVNDMLIKSCADLAVCAFPRE 383
 DB 347 --GLMISQSIKHDFKRNKMYNLTXYIDPTWIRAPSVASDNVYCTLLAQSGAHGAM--- 401
 QY 384 SGVIGHSD--NENVLRAIEPRRIKGGKPPNIDD--WFNSMLSEIQP 428
 DB 402 AGTYGYSGLVNGR-QTYIPRYRITETQNNVITDRMKAR-LLSTNQP 448

RESULT 7

Q9XL57 PRELIMINARY; PRT; 366 AA.

ID Q9XL57
 AC Q9XL57;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 6-phosphofructokinase.
 GN PFK OR CPT185.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=13 / Type A;
 RX PubMed:11792842;
 RA Shinzu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori W., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).
 DR EMBL; AP003189; BAB80891.1;
 DR InterPro; IPR000023; Pfprckinase.
 DR Pfam; PF00365; PFK; 1.
 DR PRINTS; PR00476; PHPRCKINASE.
 DR PRODOM; PD000707; Pfprckinase; 1.
 DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
 DR KINASE; Complete proteome.
 SQ SEQUENCE 366 AA; 39514 MM; C5614C41AE638C31 CRC64;

Query Match 12.2%; Score 278; DB 16; Length 366;
 Best Local Similarity 26.2%; Pred. No. 2.4e-12;
 Matches 113; Conservative 67; Mismatches 127; Indels 124; Gaps 20;

QY 28 LANKPKVAIITAGLAPCNSAIGSLERTETDPSIEIICRYGKGLLGSYPYTA 87
 DB 1 MMQPIKILILITGGDDCPGLNAVIRA-VTRAILKGYEIVIGYFGYGLYNDF--VKL 57
 QY 88 EVRRKAGVLOFGGSVIGNS-----RYKLTNVKDCVKGIVKEGDEPKVAADQVLK 139
 DB 58 DLDVSGLIHR-GSTILHSSKNKDLFDYQVDENGR-----LYK-KDVSVDVENLKK 108
 QY 140 DVVDIITIGGDDPNTAAADLAFLARNYGLTVIGLPTVNDVFPFKISGARTAAEQ 199
 DB 109 EGVVALVIGDGGTLTARDP-----SRKGVNTIGVPTIITNDLTLTVFPGNTATET 162
 QY 200 GARFPAVVAENANPMLIVHEVWGRNGMILTAAQAEYRLDLRAEWLPELGLTRESY 259
 DB 163 ATSLADRLHTAASBHHIMLT-EVWGRNAGTAL-----ESGIAASA- 203
 QY 260 EVHAFVPEPAIDLE--ABAQRLEWMDKDCVNI FVSEGA---GVFAIYAEQAKQGV 314
 DB 204 --DVILLPEIPYDINKIVKRYKEREERAGKQFTI-IYVAEAKRPDGGVVS-----KI 253
 QY 315 PDAFGHKIDAVNPGKMFGEQFAQMI GAETLVQSGYAFARASASVNDMLIKSCADL 374

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Db      254 VDSBPDRLGFI-----ANKLAIDLEG-----LTKN----- 280
Qy      375 ABECAFRESGVIGHDEHNGNV-----LRAIEPRRIKGGKPNIDTWNMSKL 422
Db      281 -----HEIRSTVLGHIOGANTSTYDRILSTKYGVKAVEL-----INSNLFGNNV 325
Qy      423 SEIGQPKGV 433
Db      326 A-----LKNKV 332

RESULT 8
ID      09AGCO      PRELIMINARY;      PRT;      341 AA.
AC      09AGCO;
DT      01-JUN-2001 (TREMBlrel. 17, Created)
DT      01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT      01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE      Phosphofructokinase-1-like protein (EC 2.7.1.11) (6-phosphofructokinase)
OS      (phosphohexokinase).
OC      Amycolatopsis mediterranei (Nocardia mediterranei).
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OX      Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
RN      NCBI_TaxID=33910;
RP      SEQUENCE FROM N.A.
RC      STRAIN=5659;
RA      Kuan L., Mueller M., August P.R., Pogoseva-Adadjanyan E., Floss H.G.,
RA      Yu T.;
RT      "Characterization and cloning of three 3-deoxy D-arabinoseputulosonate
RT      7-phosphate synthase isoenzymes from Amycolatopsis mediterranei
RT      5659."
RL      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- CATALYTIC ACTIVITY: ATP + D-FRUCTOSE 6-PHOSPHATE = ADP + D-
CC      FRUCTOSE 1,6-BISPHOSPHATE.
CC      -1- PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.
DR      EMBL; AF36847; AAC28147.1; -.
DR      HSSP; P00512; 3PFX.
DR      InterPro; IPR000023; PfRfckKinase.
DR      Pfam; PF00365; PFK. 1
DR      PRINTS; PR00476; PHFRCKTKINASE.
DR      ProDom; PD000707; PfrfckKinase; 1.
DR      PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
KW      Glycolysis; Kinase; Transferase.
SQ      SEQUENCE 341 AA; 36272 MW; 2B5C28E7BD57065 CRC64;

Query Match      12.0%; Score 274.5; DB 2; Length 341;
Best Local Similarity 26.8%; Pred. No. 3,9e-12;
Matches 101; Conservative 60; Mismatches 151; Indels 65; Gaps 15;

Qy      34 KVALITAGLAPCLNSAIGSLIERYTEIDPSIIEICVGGYKGLLGDSYPTAVRKA 93
Db      2 RGVGLVGGGCGPGLNVIKAVKGIKGV- GMPFVGRGMRNCPFLGDSRPL-GLNDVE 58
Qy      94 GYLORFGSGVIGNSRYKLVNKDCYKRGVKEGEDPQVAADQLVKGDVLIHTIGSDT 153
Db      59 DILTR-GGTILRSSRTRNPYVEGVK-1KQ-----VLADQ-----GVDALIAIGEDT 105
Qy      154 NTAADLAFLAFLANNYGLTVIGLPTVNDVDFPIKOSLGAMTAAEGAGYFNVVAENNA 213
Db      106 LGYAKKL-----TDDIGVGVKTIINDLGAFTDTPGDTAVSATAIDRLHTTAS 159
Qy      214 NPKMLIVHEVWGNCGMLTAATAOEYKRLDRAEWLPELGLTRSEYVNAVFPMAIDL 273
Db      160 HRAALTV-EVWGHHAGMIALHS-----GLAGCA-----SVILVPEHFRV 198
Qy      274 BAAKRLREVMKVDVKNIFVSEGAGVEAIVAMOKGQEV-----PDAFGHKLDAVNP 329
Db      199 DQVSWVERREFEKPAPIIVAAEGALPEG-----GEKKLTGKDAFGVRLGGI-- 248
Qy      330 GKAFGRQPAOMIAGKTLVQKSGYFARASAVNDVMLIKSCADLAVEGAFRESGVIGH 389

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Db      249 GTWLADEIAHRTGKSRAN-VLGHVQKGTPTAHYRVLATRTPLGLNANVADGDFGVM-- 305
Qy      390 DEBNGNVIAIEFPRIK 406
Db      306 -----VALKGTDIVRVK 317

RESULT 9
ID      051669      PRELIMINARY;      PRT;      448 AA.
AC      051669;
DT      01-JUN-1998 (TREMBlrel. 06, Created)
DT      01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Pyrophosphate--fructose 6-phosphate 1-phosphotransferase (PFK).
OS      BB0727.
OC      Borrelia burgdorferi (Lyme disease spirochete).
OC      Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX      NCBI_TaxID=139;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 35210 / B31;
RX      MEDLINE=98065943; PubMed=9403685;
RA      Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA      Iathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA      Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Hanson M.,
RA      Peterson U., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA      van Vugt R., Palmer N., Adams M.D., Gockayne J.D., Weiman J.,
RA      Garland S., Fujii C., Cotton M.D., McDonald L., Artlich P., Bowman C.,
RA      Smith R.O., Venter J.C.;
RT      "Genomic sequence of a Lyme disease spirochete, Borrelia
RT      burgdorferi."
RL      Nature 390:580-586(1997).
DR      EMBL; AS001172; AAC67070.1; -.
DR      HSSP; P00512; 3PFX.
DR      TIGR; BB0727; -.
DR      InterPro; IPR000023; PfrfckKinase.
DR      Pfam; PF00365; PFK. 1.
DR      PRINTS; PR00476; PHFRCKTKINASE.
DR      ProDom; PD000707; PfrfckKinase; 1.
KW      Transferase; Complete proteome.
SQ      SEQUENCE 448 AA; 49887 MW; A4BA292360032D51 CRC64;

Query Match      11.8%; Score 270; DB 16; Length 448;
Best Local Similarity 24.9%; Pred. No. 1.3e-11;
Matches 102; Conservative 69; Mismatches 177; Indels 62; Gaps 11;

Qy      34 KVALITAGLAPCLNSAIGSLIERYTEIDPSIIEICVGGYKGLLGDSYPTAVRKA 93
Db      81 KKAITTCGLCPGFNDVRSIVRTLMKIYGVNIIYGVKYGGLPSSNSPTININPQV 140
Qy      94 GYLORFGSGVIGNSRYKLVNKDCYKRGVKEGEDPQVAADQLVKGDVLIHTIGSDT 153
Db      141 DDINRFGTILGSS-----RGKIPV-----IYDTERNNIMNMFNIGSGGT 183
Qy      154 NTAADLAFLAFLANNYGLTVIGLPTVNDVDFPIKOSLGAMTAAEGAGYFNVVAENNA 213
Db      184 QKGSLLIABEIERKRLKAVVGIPTVNDVDFPVKSGGFETAVQVAAVAGAFKANS 243
Qy      214 NPKMLIVHEVWGNCGMLTAATAOEYKRLDRAEWLPELGLTRSEYVNAVFPMAIDL 273
Db      244 AVNGIGLVKVMGRSGFLAHTA-----LSSNDVFCILPELDPI 284
Qy      274 EAE-----AKEL-REVMKVDVKNIFVSEGAGVEAIVAMOKGQEV-----PDAFGH 322
Db      285 EGPNGFTVHLERRLIKESLIERIPHAVLIIAGAG-----OKYFHFPRKKDSSNL 336
Qy      333 KLDVNPGRKMFGBQAFQMTGAEK--TLVQ-KSGYFARASAVNDVMLIKSCADLAVEC 378
Db      337 LYEDI--GLYIKDKITEYKAKNIOFTLKYIDPSYIISSPANAASDSIYCARLSNAVHA 394
Qy      379 AFRESGVIGHDEHNGNVIAIEFPRIKGGKPNIDTWNMSLSEIQP 428

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Db 395 AAGAGTKMLISLMSTKFEVPIKKAVIDRNR-VNPGSGFMRDVLSTGQP 443

RESULT 10

ID 094AA4 PRELIMINARY: PRT: 489 AA.

AC 094AA4: 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE AT4946270/T25K17.80.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC OC Brasicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bower L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai U., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Natusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RA "Arabidopsis cDNA clones";
 RT Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Meyers M.C., Shinn P., Banh J.,
 RA Bower L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai U., Lam B., Lee J.M., Lin J., Miranda M., Natusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RA "Arabidopsis ORF clones";
 RT Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EMBL: AY049245; AK83587.1; -
 DR EMBL: AY090267; AAL90928.1; -
 DR InterPro: IPR000023; Pfriuckinase.
 DR Pfam: PF00365; PFK; 1.
 DR PRINTS: PR00476; PFRCKTNASE.
 DR ProDom: PD000707; Pfruckinase; 1.
 SQ SEQUENCE 489 AA; 53666 MW; A82C1EAI5B64F7B0 CRC64;

Query Match 11.6%; Score 266; DB 10; Length 489;

Best Local Similarity 25.7%; Pred. No. 2.9e-11;

Matches 105; Conservative 61; Mismatches 172; Indels 70; Gaps 13;

QY 37 ILTAGLAPCLNSAIGSLIRYETIDPSIILICRGYKGLLDSDSYVLAFAVKKXGVL 96
 DB 96 IVFCGGLCPGLNVTREIVSLSVYGVKRLIGIDGGRGYAKNTVSLDSKV--VNDI 152
 QY 97 QRFSGSVIGNSRVKLTNYKDCVKGGLVKEGEDPKQVADQLVKDGVDLHTIGDDTNTA 156
 DB 153 HKGGTILIGTSR-----GHDITKRL-VDSIDRGINGVYIIGDDGORG 195
 QY 157 AADLAFLAARNNGELTVIGLPTVDNDVFPFKQSIGANTAAEQGAKRFANVVAENANPR 216
 DB 196 ASVIFEEIRRRGLKAAVIGIPRTIDNDIPVDFKSGFPTAAVEAQRALNAHVAESIEIN 255
 QY 217 MLIVHEVGRNCGMLTAATAOEYRKLDRAMLELDELGTRESYEVAHVFVEMAIIDEAE 276
 DB 256 GIGVYKLMGRYSGLFA-----MATTASRVYDCCILPESFYIEGE 296
 QY 277 A-----KLRVWDKVDKCNITFVSGAGVBAVAENQAGQGVPRDAGHITLADVNP 329
 DB 297 GGLPEYIERKRLKESGHNV-----LVTAAGQDILMSKSMESW--TLXDASGNKILKDV-- 347

QY 330 GKPFGEQPAOMTGAETLVQ---KSGYFAPASASNDVDELLKSCADLAVECAFRESG 385
 DB 348 GLMWSQIKDHFNOKKKVMMLKYIDPTYMIRAVPSNADSVYCYTLAQSAVHGMAGYTG 407
 QY 386 VIGHDEEDGNV---LRAIEFPRIKGGKPFNIDTD--WFNSMLSEIGQP 428
 DB 408 YI-----SGLVNGRQTYIPYRILTEKONHAYVIDRMRAR-LISSTNQP 449

RESULT 11

ID 027651 PRELIMINARY: PRT: 436 AA.

AC 027651: 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Pyrophosphate-fructose-6-phosphate 1-phosphotransferase
 DE (EC 2.7.1.90).
 GN EH/PPI-PFK.
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=5759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINB=96235172; PubMed=8645233;
 RX Bruchhaus I., Jacobs T., Denart M., Tannich E.;
 RA "Pyrophosphate-dependent phosphofructokinase of Entamoeba histolytica:
 RT molecular cloning, recombinant expression and inhibition by
 RT pyrophosphate analogues";
 RL Biochem. J. 316:57-63 (1996).
 DR EMBL: X82173; CA57659.1; -
 DR HSPG: P00512; 3PEK.
 DR InterPro: IPR000023; Pfruckinase.
 DR Pfam: PF00365; PFK; 1.
 DR PRINTS: PR00476; PFRCKTNASE.
 DR ProDom: PD000707; Pfruckinase; 1.
 KW Transferrase.
 SQ SEQUENCE 436 AA; 47571 MW; 1CECCFC05DC8D63 CRC64;

Query Match 11.5%; Score 263.5; DB 5; Length 436;

Best Local Similarity 26.3%; Pred. No. 3.7e-11;

Matches 108; Conservative 68; Mismatches 164; Indels 71; Gaps 16;

QY 34 KVALITAGLAPCLNSAIGSLIRYETIDPSIILICRGYKGLLDSDSYVLAFAVKKXGVL 91
 DB 82 KVALITAGLAPCLNSAIGSLIRYETIDPSIILICRGYKGLLDSDSYVLAFAVKKXGVL 139
 QY 92 KAGVLPFGSGSVIGNSRVKLTNYKDCVKGGLVKEGEDPKQVADQLVKDGVDLHTIGDD 151
 DB 140 -VSDIHQKGGSLIGTSR-----GAQSPVMAQFLIDNNFNILFTLIGD 181
 QY 152 DITTAADLAFLAARNNGELTVIGLPTVDNDVFPFKQSIGANTAAEQGAKRFANVVAENANPR 211
 DB 182 GLTAKGNAINKELRRKRPVTVIGIPRTIDNDICYTDSIFGPTAVAGLSGEALNAHVAESIEIN 241
 QY 212 NANPRMLIVHEVGRNCGMLTAATAOEYRKLDRAMLELDELGTRESYEVAHVFVEMAI 271
 DB 242 KSAKNGSIGVYRLMRGRAGFIAL-----VASLANG-----DANVLIDIEIDI 282
 QY 272 DL-----EAAKRLREVDNDVFNITFVSGAGVBAVAENQAGQGVPRDAGHITLADVNP 326
 DB 283 PITQICEFQGR--IMSKGHV-IYVABGA-----LQNKRPDLDLGDKSNILHWS 333
 QY 327 VNEGKMGGEQPAOMTGAETLVQ---KSGYFAPASASNDVDELLKSCADLAVECAFRESG 384
 DB 334 INTLRISITLYKLSIIEHTITKTFVPSYMRISAPCSAADAHFCMLANAAVAVAMAGKT 393
 QY 385 G-VIGHDEEDGNVLAIEFPR-----IKGKPFNIDTD--WFNSMLSEIGQP 429
 DB 394 GLVTCGHNNH--FVSVPIDRTSYIK-----RVNDGSLYTWMSAIEPK 436

RESULT 12

094J12 PRELIMINARY: PRT: 586 AA.

ID 094J12
AC 094J12
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Putative pyrophosphate--fructose-6-phosphatet
DE Putative pyrophosphate--fructose-6-phosphatet
DE phosphotransferase)
GN P0638D12.7 OR OSUNB0021A09.21.
OS Oryza sativa (Rice), and
OC Oryza sativa [japonica cultivar-group].
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriodes; Oryzae; Oryza.
OX NCBI_TaxID=4530, 39947;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0638D12.7";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
RT clone: OSUNB0021A09.21";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003218; BAB5949.1; -
DR EMBL; AP003218; BAB5949.1; -
DR Gramene; O94J12; -
DR InterPro; IPR000023; Pfufuckinase.
DR Pfam; PF00365; PFK; 1.
DR PRINTS; PR00476; PHFRCKINASE.
DR PRODOM; PD000707; Pfruckinase; 1.
DR TRANSFERASE.
KW SEQUENCE 586 AA; 64060 MW; 28DE4F800386A3 CRC64;

Query Match 11.5%; Score 263.5; DB 10; Length 586;
Best Local Similarity 26.2%; Pred. No. 5.9e-11;
Matches 96; Conservative 53; Mismatches 158; Indels 59; Gaps 9;

QY 34 KVALTAGAPCLNSAIGSLIERYTEIDSEIILICRGYKGLLDGSPYVAEYKKA 93
DB 189 KACIVTCGGLCPGINTVIRLVOSLSHMYVNDIFGIQNGYKGFYSNTYLPMP--KSY 245
QY 94 CVLORFGGSVIGNSRVKLTNVKDCVKGGLYKGBDPOKVAADQLVKGDVLIHTIGDDT 153
DB 246 NDHHRGGTVLGTSR-----GGHDTGKI-VDMICGRGINQVYIIGDDGT 288
QY 154 NTAADLAATLARNNGVLTIGLPTVNDVFPFKOSLGAMTAAGGARFMMVVAENNA 213
DB 289 QKARVETKIRRGKLVAAAGPKIINDIAVIDSGFDSVVEKQRIIDAAHVEASS 348
QY 214 NPMALIVHEVWGRNGCMTAATAQBYRKLDRAEWLPELGLITRESEYVNAVFPEMAID 273
DB 349 AENGIGVLMKRGYSPTA-----MYATLASRDVDCCLIPSPFPFL 389
QY 274 EABA-----KLEBEMDVDCNIFVSEAGAVEAIVAEQAKGSEPRDAFGHIKLDVA 326
DB 390 EGGGLFEYIEKRLKENNHV-----IVVAEGAQODLIASIAAAD--IDSAGNLL-- 440
QY 327 VNPGRFGGQFAOMIGAELTVQ-----KSGYFARASASVNDRLIKSCADILAVECAFR 382
DB 441 LDVGLVLTIRIKOYCKNKKEMTIKVIDPTVYIRALPSNASDNVYCTLLAHSIHGAAMG 500
QY 383 ESGVIG 388
DB 501 YSFTVG 506

RESULT 13

Q91G72 PRELIMINARY: PRT: 775 AA.

ID Q91G72
AC Q91G72
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Putative pyrophosphate-dependent phosphofructo-1-kinase.
DE Putative pyrophosphate-dependent phosphofructo-1-kinase.
GN P0710E05.25 OR P0671B11.1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriodes; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. NIPPONBAR;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0710E05.25";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0671B11.1";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002743; BAA9438.1; -
DR EMBL; AP002746; BAA12686.1; -
DR HSP; P00512; 3PFK.
DR Gramene; O91G72; -
DR InterPro; IPR000023; Pfruckinase.
DR InterPro; IPR000634; S/T_denydrtse.
DR Pfam; PF00365; PFK; 1.
DR PRINTS; PR00476; PHFRCKINASE.
DR PRODOM; PD000707; Pfruckinase; 1.
DR PROSITE; PS00165; DEHYDRATASE_SBR_THR; 1.
KW KINASE.
KW SEQUENCE 775 AA; 84371 MW; B4390F7D8A9C907A CRC64;

Query Match 11.4%; Score 260.5; DB 10; Length 775;
Best Local Similarity 26.2%; Pred. No. 1.5e-10;
Matches 107; Conservative 54; Mismatches 180; Indels 67; Gaps 13;

QY 36 ALTAGAGAPCLNSAIGSLIERYTEIDSEIILICRGYKGLLDGSPYVAEYKKA 95
DB 374 ALVTGGLCPGINTVIRLVOSLSHMYVNDIFGIQNGYKGFYSNTYLPMP--KSY 245
QY 96 LORFGGSVIGNSRVKLTNVKDCVKGGLYKGBDPOKVAADQLVKGDVLIHTIGDDT 155
DB 431 IHKRGTVLGTSR-----GGHDTGKI-VDSIKDGINQVYIIGDDGT 473
QY 156 AAADLAATLARNNGVLTIGLPTVNDVFPFKOSLGAMTAAGGARFMMVVAENNA 215
DB 474 GASVIFQEVRRRGLKCSVGVYKPTINDIQVIDKSGFGEPTVAEBQRIIDAAHVEASS 533
QY 216 RMLIVHEVWGRNGCMTAATAQBYRKLDRAEWLPELGLITRESEYVNAVFPEMAID 275
DB 534 NGIGVLMKRGYSPTA-----MYATLASRDVDCCLIPSPFPFL 389
QY 276 EA-----KLEBEMDVDCNIFVSEAGAVEAIVAEQAKGSEPRDAFGHIKLDVA 328
DB 575 KGLLEFTEKRLKDNHNV-----IVVAEGAQODLIASIAAAD--IDSAGNLL--LD 625
QY 329 PKMFGGQFAOMIGAELTVQ-----VQSGYFARASASVNDRLIKSCADILAVECAFR 383
DB 626 VGLMLSQIKDHFKKRFPITTKIIDPTVYIRALPSNASDNVYCTLLAHSIHGAAMG 500
QY 384 SGVIGHDEDNNGVLR--IEPPI--KGGKPPNIDTWNSMLSEIGOP 428
DB 683 AGYGFVAAPVNGRAVYIPFYRIKTEKQKVVITTRMMAR-VLCSTNQP 729


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RESULT 14
ID Q24812 PRELIMINARY; PRT; 382 AA.
AC Q24812;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE PPI-dependent phosphofructo-1-kinase (EC 2.7.1.90).
GN PFK.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95143279; PubMed=7841199;
RA Huang M., Altsch R.A., Chang K.P., Kemp R.G.,
RT "Cloning and sequencing a putative pyrophosphate-dependent
RT phosphofructokinase gene from Entamoeba histolytica."
RL Biochim. Biophys. Acta 1260:215-217 (1995).
DR EMBL; U12513; AAA2671.1; -.
DR HSSP; P00512; 3PFK.
DR InterPro; IPR000023; Pfrckinase.
DR Pfam; PF00365; PFK; 1.
DR PRINTS; PR00476; PFRCKTNASE.
DR ProDom; PD000707; Pfrckinase; 1.
DR Kinease; Transferase.
SQ SEQUENCE 382 AA; 41747 MW; 7ECCEBP37CD4F87B CRC64;

Query Match 11.4%; Score 260; DB 5; Length 382;
Best Local Similarity 26.7%; Pred. No. 5.5e-11;
Matches 99; Conservative 63; Mismatches 149; Indels 60; Gaps 14;

QY 34 KVALITAGLAQCLNSAI GSIERYTEIDPSIRHICRGGYKLL LGDSYPTAAVR 90
DB 37 KVALITCGGLCPGLNNVIRGLVLTNRYHYV-NIPGLRWGYEGVLPUSVQRTPRI 94
QY 91 KKAQVLORFQSGSVIGNSRVKLTNVDCVRGLVKEGEDPOKVAADQLVKGVDLHTTIG 150
DB 95 --VSDIHQGGSIILGTSR-----GAQSPVMAQFLDNNNNILFTLGG 135
QY 151 DDTNTAAADLAAFLARNYGLTVIGLPTVNDVPIKOSLGAMTAAQAGARYFNVAE 210
DB 136 DDTLGAANAINKELRRKVPITVVGIPKTIIDNDIYDTSTFGFTAVGLSGEAINVAHSE 195
QY 211 NNANRPMILVHVMGRNCGMLTAATAQGYRKLIDRAEWLPBELGLTRSEYHAAVFPKMA 270
DB 196 AKSAGKGIQIVLMGRDGFIAL-----YASLANG-----DANVILIPID 236
QY 271 IDL---EAAKRLBVDKVDVNI FVSEGAGVEAIVAEQAKQGVPRDAFGHI-KLD 325
DB 237 IPIITGICEFVGKR--IMSKGHV-IVVAEGA-----LONQPKOLDIGTDSGIIITMD 287
QY 326 ANPPKMPGBOFAOMIGAEKTLVQ--KSGYFARASASVNDRLKSGADLAVECAFRR 383
DB 288 SNNYRDSITTKLKGSTIGIEHTIKFVDPSYIMRSAPCSADAHFPCCLANAAVHVAAMGK 347
QY 384 SG-VIGHEDN 393
DB 348 TGLVICHNN 358

RESULT 15
ID Q9STQ7 PRELIMINARY; PRT; 500 AA.
AC Q9STQ7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Pyrophosphate-dependent phosphofructo-1-kinase.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Beyan M., Koeltter P., Entian K.-D., Bancroft I.,
RA Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049171; CAB38956.1; -.
DR EMBL; AL049171; CAB38956.1; -.
DR HSSP; P00512; 3PFK.
DR InterPro; IPR000023; Pfrckinase.
DR Pfam; PF00365; PFK; 1.
DR PRINTS; PR00476; PFRCKTNASE.
DR ProDom; PD000707; Pfrckinase; 1.
DR Kinease.
SQ SEQUENCE 500 AA; 55295 MW; A09DF850C905087 CRC64;

Query Match 11.3%; Score 257.5; DB 10; Length 500;
Best Local Similarity 25.6%; Pred. No. 1.3e-10;
Matches 109; Conservative 59; Mismatches 167; Indels 91; Gaps 16;

QY 37 ILTNGGLAPCLNSAISL-----ISRYTEIDPSIRHIC-----YRGYGL 78
DB 92 ILTNGGLCPGLNVIIRIVSLSYMGVKRIIGDVS--FDCNLLITNTNGYGFY 148
QY 79 LGDSYPTAAVRKKAQVLORFQSGSVIGNSRVKLTNVDCVRGLVKEGEDPOKVAADQLV 138
DB 149 AKNTVSDSKV---VNDIHQGGSIILGTSR-----GHDITTKI-VDSIQ 168
QY 139 KQGVILHTTGGDDTNTAAADLAAFLARNYGLTVIGLPTVNDVPIKOSLGAMTAAE 196
DB 189 DRGINQYIIIGDGTORAGACVIEEIRIRRLKVAVIGIPKTIIDNDIYDIDKSFQFVAE 248
QY 199 OGARYFNVAEANNANRPMILVHVMGRNCGMLTAATAQGYRKLIDRAEWLPBELGLTRSE 258
DB 249 EAQDAITAAHVAEASINSTNGIGVAKMKRYSGFLA-----MYATLAS 289
QY 259 YEVHAAVPEMAIDLEAE-----KRLREVNDKVDVNI FVSEGAGVEAIVAEQAKG 311
DB 290 RDVDCCLIPSPFYLBSGGLFYIEKRLRESGHV--LVIAEGGQDILMSKSMESM- 344
QY 312 QEVPRDAFGHIKLDVAVPGKPRGPAQMTIGAEKTLVQ--KSGYFARASASVNDRL 367
DB 345 --TLKQASGNKLLDV--GLMSQSTIKDHPNOKKVMNLYKTIPTTIRVPSNASDNY 400
QY 368 IKSCADLAVCAFRRESGVIGHEDNGNV--LRAIEFPRIKQKPFNIDT--WFNSML 422
DB 401 CTLAQAAGVAGAAVGYI-----SGLVNGRGQTYIFFYRITRKONHVITDRMMAR-LL 454
QY 423 SRIQOP 428
DB 455 SSTNQP 460

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Search completed: January 29, 2004, 14:37:55
 Job time : 43 secs

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OM protein - protein search, using sw model

Run on: January 29, 2004, 14:37:58 ; Search time 39 Seconds
(Without alignments)
2328.635 Million cell updates/sec

Title: US-09-941-947A-2
Perfect score: 2284
Sequence: 1 DVTWTFYHLTADIRFCWTF.....FNSMSEIQPKGKIVSH 437

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 789580 seqs, 207824079 residues
Total number of hits satisfying chosen parameters: 789580

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

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Database:

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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2284	100.0	437	10	US-09-934-901-16
2	2284	100.0	437	10	US-09-934-868-6
3	2284	100.0	437	11	US-09-941-947A-2
4	2284	100.0	437	12	US-10-320-874-16
5	2284	100.0	437	16	US-10-320-924-16
6	659	28.9	184	12	US-10-369-493-14348
7	306.5	13.4	350	12	US-10-369-493-8108
8	294	12.9	342	15	US-10-156-761-13610
9	284.5	12.5	341	15	US-10-156-761-14652
10	269.5	11.8	341	15	US-10-156-761-10355
11	261	11.4	345	12	US-10-369-493-18261
12	250.5	11.1	319	12	US-10-369-493-2905
13	246.5	10.8	357	12	US-10-369-493-9669
14	246.5	10.8	987	12	US-10-369-493-21998
15	240.5	10.5	320	9	US-09-815-242-13785

16	239.5	10.5	318	12	US-10-369-493-9652	Sequence 9652, Ap
17	238.5	10.4	320	9	US-09-815-242-10422	Sequence 10422, A
18	238.5	10.4	320	12	US-10-369-493-23638	Sequence 23638, A
19	229.5	10.0	295	12	US-10-369-493-8855	Sequence 8855, Ap
20	227.5	10.0	449	12	US-10-369-493-8876	Sequence 8876, Ap
21	226.5	9.9	320	9	US-09-815-242-11721	Sequence 11721, A
22	224.5	9.8	334	12	US-10-369-493-515	Sequence 515, App
23	223.5	9.7	319	12	US-10-369-493-17399	Sequence 17399, A
24	222.5	9.7	322	9	US-09-815-242-5425	Sequence 5425, Ap
25	222.5	9.7	322	9	US-09-815-242-12619	Sequence 12619, A
26	222.5	9.7	322	9	US-09-815-242-12907	Sequence 12907, A
27	222.5	9.7	360	12	US-10-369-493-19198	Sequence 19198, A
28	222	9.7	322	12	US-10-369-493-10132	Sequence 10132, A
29	222	9.7	340	12	US-10-369-493-18431	Sequence 18431, A
30	221	9.7	335	9	US-09-815-242-13346	Sequence 13346, A
31	218.5	9.6	320	9	US-09-815-242-10649	Sequence 10649, A
32	215	9.4	321	12	US-10-369-493-21210	Sequence 21210, A
33	213.5	9.3	321	12	US-10-369-493-128	Sequence 128, App
34	213	9.3	321	12	US-10-369-493-479	Sequence 479, App
35	207	9.1	959	12	US-10-369-493-1903	Sequence 1903, Ap
36	202.5	8.9	321	9	US-09-815-242-11162	Sequence 11162, A
37	201.5	8.8	361	12	US-10-369-493-2625	Sequence 2625, Ap
38	201	8.8	343	9	US-09-887-054-2	Sequence 2, Appli
39	201	8.8	343	15	US-10-098-626-2	Sequence 2, Appli
40	201	8.8	357	10	US-09-738-626-4883	Sequence 4883, Ap
41	200	8.8	776	15	US-10-205-342-5	Sequence 5, Appli
42	198	8.7	419	12	US-10-369-493-5919	Sequence 5919, Ap
43	196	8.6	321	12	US-10-369-493-10434	Sequence 10434, A
44	196	8.6	828	12	US-10-369-493-6730	Sequence 6730, Ap
45	193	8.5	942	12	US-10-369-493-2497	Sequence 2497, Ap

ALIGNMENTS

RESULT 1
US-09-934-901-16
Sequence 16, Application US/0934901
Parent No. US20020110885A1
GENERAL INFORMATION:
APPLICANT: Kodas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: No. US20020110885A1ton, Kelley C.
APPLICANT: Ye, Rick
TITLE OF INVENTION: DENTRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: C1619 US NA
CURRENT APPLICATION NUMBER: US/09/934,901
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,906
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Office 97
SEQ ID NO 16
LENGTH: 437
TYPE: PRT
ORGANISM: METHYLOMONAS SP.
US-09-934-901-16

Query Match	Similarity	Score	DB ID	Length	Matches	Local	Conservative	Mismatches	Indels	Gaps
1	100.0%	2284	10	437	437	437	0	0	0	0
2	100.0%	2284	10	437	437	437	0	0	0	0
3	100.0%	2284	10	437	437	437	0	0	0	0
4	100.0%	2284	10	437	437	437	0	0	0	0
5	100.0%	2284	10	437	437	437	0	0	0	0
6	28.9	659	12	184	184	184	0	0	0	0
7	13.4	306.5	12	350	350	350	0	0	0	0
8	12.9	294	15	342	342	342	0	0	0	0
9	12.5	284.5	15	341	341	341	0	0	0	0
10	11.8	269.5	15	341	341	341	0	0	0	0
11	11.4	261	12	345	345	345	0	0	0	0
12	11.1	250.5	12	319	319	319	0	0	0	0
13	10.8	246.5	12	357	357	357	0	0	0	0
14	10.8	246.5	12	987	987	987	0	0	0	0
15	10.5	240.5	9	320	320	320	0	0	0	0

QY 181 DNDVFPKISLGAMTAAGARFEMNVVAENNANPRLTVEHVGKNCGLTAAATQBYR 240
 DB 181 DNDVFPKISLGAMTAAGARFEMNVVAENNANPRLTVEHVGKNCGLTAAATQBYR 240
 QY 241 KLDRAEWLPELGLTRESYEVHAFVPEMAIDLEAAKRLREVMDCVNI FVSEAGAV 300
 DB 241 KLDRAEWLPELGLTRESYEVHAFVPEMAIDLEAAKRLREVMDCVNI FVSEAGAV 300
 QY 301 EALVAEMQAKQGVPRDAPFGHILKIDAVNPGKMFGEOPACMIGAEKTLVQKSGYFARASAS 360
 DB 301 EALVAEMQAKQGVPRDAPFGHILKIDAVNPGKMFGEOPACMIGAEKTLVQKSGYFARASAS 360
 QY 361 NVDDMRLLKSCADLAVECAFRRESGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMFNS 420
 DB 361 NVDDMRLLKSCADLAVECAFRRESGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMFNS 420
 QY 421 MUSEIGOPKGGKVEVSH 437
 DB 421 MUSEIGOPKGGKVEVSH 437

RESULT 2

US-09-934-868-6
 ; Sequence 6, Application US/09934868
 ; Patent No. US20020137190A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kofidas, Mattheos
 ; APPLICANT: Odum, James M
 ; APPLICANT: Schenzle, Andreas J
 ; TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
 ; FILE REFERENCE: C11596 US NA
 ; CURRENT APPLICATION NUMBER: US/09/934, 868
 ; CURRENT FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 60/229, 858
 ; PRIOR FILING DATE: 2000-09-01
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 6
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: METHYLOMONAS SP.
 ; US-09-934-868-6

Query Match 100.0%; Score 2284; DB 10; Length 437;

Best Local Similarity 100.0%; Pred. No. 1,4e-223; Indels 0; Gaps 0;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVTWPFYHLTADIRFCHEFLNFNFTLNMKPKKVALITAGGLAPCLNSAIGSLIERYTE 60
 DB 1 DVTWPFYHLTADIRFCHEFLNFNFTLNMKPKKVALITAGGLAPCLNSAIGSLIERYTE 60
 QY 61 IDPSIEIICRYGGYKGLIGDSYPTAEVRKKAQVLRFGSGVIGNSRKLTVNDQCYR 120
 DB 61 IDPSIEIICRYGGYKGLIGDSYPTAEVRKKAQVLRFGSGVIGNSRKLTVNDQCYR 120
 QY 121 GLVXGEGDPQKVAADQVLDVGDVILHTIGDDTNTAAADLAFLARNNYGLTVIGLPTV 180
 DB 121 GLVXGEGDPQKVAADQVLDVGDVILHTIGDDTNTAAADLAFLARNNYGLTVIGLPTV 180
 QY 181 DNDVFPKISLGAMTAAGARFEMNVVAENNANPRLTVEHVGKNCGLTAAATQBYR 240
 DB 181 DNDVFPKISLGAMTAAGARFEMNVVAENNANPRLTVEHVGKNCGLTAAATQBYR 240
 QY 241 KLDRAEWLPELGLTRESYEVHAFVPEMAIDLEAAKRLREVMDCVNI FVSEAGAV 300
 DB 241 KLDRAEWLPELGLTRESYEVHAFVPEMAIDLEAAKRLREVMDCVNI FVSEAGAV 300
 QY 301 EALVAEMQAKQGVPRDAPFGHILKIDAVNPGKMFGEOPACMIGAEKTLVQKSGYFARASAS 360
 DB 301 EALVAEMQAKQGVPRDAPFGHILKIDAVNPGKMFGEOPACMIGAEKTLVQKSGYFARASAS 360
 QY 361 NVDDMRLLKSCADLAVECAFRRESGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMFNS 420
 DB 361 NVDDMRLLKSCADLAVECAFRRESGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMFNS 420

DB 361 NVDDMRLLKSCADLAVECAFRRESGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMFNS 420
 QY 421 MUSEIGOPKGGKVEVSH 437
 DB 421 MUSEIGOPKGGKVEVSH 437

RESULT 3

US-09-941-947a-2
 ; Sequence 2, Application US/09941947a
 ; Publication No. US2003003528A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brzostowicz, Patricia C.
 ; APPLICANT: Cheng, Qiong
 ; APPLICANT: DiCosimo, Deana J.
 ; APPLICANT: Kofidas, Mattheos
 ; APPLICANT: Miller, Edward S. Jr.
 ; APPLICANT: Odum, J. Martin
 ; APPLICANT: Picataggio, Steve
 ; APPLICANT: Rovielle, Pierre E.
 ; TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
 ; FILE REFERENCE: C11903 US NA
 ; CURRENT APPLICATION NUMBER: US/09/941,947a
 ; CURRENT FILING DATE: 2001-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,907
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,858
 ; PRIOR FILING DATE: 2000-09-01
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 2
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Methylomonas 16a
 ; US-09-941-947a-2

Query Match 100.0%; Score 2284; DB 11; Length 437;

Best Local Similarity 100.0%; Pred. No. 1,4e-223; Indels 0; Gaps 0;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVTWPFYHLTADIRFCHEFLNFNFTLNMKPKKVALITAGGLAPCLNSAIGSLIERYTE 60
 DB 1 DVTWPFYHLTADIRFCHEFLNFNFTLNMKPKKVALITAGGLAPCLNSAIGSLIERYTE 60
 QY 61 IDPSIEIICRYGGYKGLIGDSYPTAEVRKKAQVLRFGSGVIGNSRKLTVNDQCYR 120
 DB 61 IDPSIEIICRYGGYKGLIGDSYPTAEVRKKAQVLRFGSGVIGNSRKLTVNDQCYR 120
 QY 121 GLVXGEGDPQKVAADQVLDVGDVILHTIGDDTNTAAADLAFLARNNYGLTVIGLPTV 180
 DB 121 GLVXGEGDPQKVAADQVLDVGDVILHTIGDDTNTAAADLAFLARNNYGLTVIGLPTV 180
 QY 181 DNDVFPKISLGAMTAAGARFEMNVVAENNANPRLTVEHVGKNCGLTAAATQBYR 240
 DB 181 DNDVFPKISLGAMTAAGARFEMNVVAENNANPRLTVEHVGKNCGLTAAATQBYR 240
 QY 241 KLDRAEWLPELGLTRESYEVHAFVPEMAIDLEAAKRLREVMDCVNI FVSEAGAV 300
 DB 241 KLDRAEWLPELGLTRESYEVHAFVPEMAIDLEAAKRLREVMDCVNI FVSEAGAV 300
 QY 301 EALVAEMQAKQGVPRDAPFGHILKIDAVNPGKMFGEOPACMIGAEKTLVQKSGYFARASAS 360
 DB 301 EALVAEMQAKQGVPRDAPFGHILKIDAVNPGKMFGEOPACMIGAEKTLVQKSGYFARASAS 360
 QY 361 NVDDMRLLKSCADLAVECAFRRESGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMFNS 420
 DB 361 NVDDMRLLKSCADLAVECAFRRESGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMFNS 420
 QY 421 MUSEIGOPKGGKVEVSH 437
 DB 421 MUSEIGOPKGGKVEVSH 437

RESULT 4
US-10-320-874-16
Sequence 16, Application US/10320874
Publication No. US20030138909A1
GENERAL INFORMATION:
APPLICANT: Odom, J. Matheos
APPLICANT: Odom, J. Matheos
APPLICANT: No. US20030138909A1, Kelley C.
APPLICANT: Ye, Rick
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: C1619 US NA
CURRENT APPLICATION NUMBER: US/10/320,874
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US/09/934,901
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,906
PRIOR FILING DATE: September 1, 2000
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Office 97
SEQ ID NO 16
LENGTH: 437
TYPE: PRF
ORGANISM: METHYLOMONAS SP.
US-10-320-874-16

Query Match 100.0%; Score 2284; DB 12; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.4e-223;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVTWPHLTADIRFCHEFLNENFYTLNMPKPKVAILTAGGLAPCLNSAIGSLIRYTE 60
DB 1 DVVTWPHLTADIRFCHEFLNENFYTLNMPKPKVAILTAGGLAPCLNSAIGSLIRYTE 60
QY 61 IDPSIRILCYRGYKGLLDGSDYPTAEVRKAGVLRFGGSVIGNSRVLTNVKDCVCR 120
DB 61 IDPSIRILCYRGYKGLLDGSDYPTAEVRKAGVLRFGGSVIGNSRVLTNVKDCVCR 120
QY 121 GLVGEEDPQKVAADQVLDGVDILHTIGDDTNTAAADLAFLANNYGLTVIGLPTV 180
DB 121 GLVGEEDPQKVAADQVLDGVDILHTIGDDTNTAAADLAFLANNYGLTVIGLPTV 180
QY 121 GLVGEEDPQKVAADQVLDGVDILHTIGDDTNTAAADLAFLANNYGLTVIGLPTV 180
DB 121 GLVGEEDPQKVAADQVLDGVDILHTIGDDTNTAAADLAFLANNYGLTVIGLPTV 180
QY 181 DNDVPIKOSLGAMTAABOGARYFMNVVAENNANPRLIVHEVMGNCGLTAATQCYR 240
DB 181 DNDVPIKOSLGAMTAABOGARYFMNVVAENNANPRLIVHEVMGNCGLTAATQCYR 240
QY 241 KLDRAEMLPELGLTRESYEVAHVPVEMALIDAEAKRLREVMQKDCVNIIVSSGAGV 300
DB 241 KLDRAEMLPELGLTRESYEVAHVPVEMALIDAEAKRLREVMQKDCVNIIVSSGAGV 300
QY 301 EAIVAEMQAKGQEVPRDAFGHILKDAVNPGRMGEOFAOMIGAEXTLVOKSGYFARASAS 360
DB 301 EAIVAEMQAKGQEVPRDAFGHILKDAVNPGRMGEOFAOMIGAEXTLVOKSGYFARASAS 360
QY 361 NVDNMLIKSCADLAVECAFRESGVIGHEDNNGNTLRAIEPRIRKGRPFNIDTMFNS 420
DB 361 NVDNMLIKSCADLAVECAFRESGVIGHEDNNGNTLRAIEPRIRKGRPFNIDTMFNS 420
QY 421 MLESIQPKGKGVESH 437
DB 421 MLESIQPKGKGVESH 437

RESULT 5
US-10-320-924-16
Sequence 16, Application US/1036924
Publication No. US20030129721A1
GENERAL INFORMATION:
APPLICANT: Koffas, Matheos
APPLICANT: Odom, J. Matheos
APPLICANT: No. US20030129721A1, Kelley C.
APPLICANT: Ye, Rick
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

FILE REFERENCE: C1619 US NA
CURRENT APPLICATION NUMBER: US/10/320,924
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US/09/934,901
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,906
PRIOR FILING DATE: September 1, 2000
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Office 97
SEQ ID NO 16
LENGTH: 437
TYPE: PRF
ORGANISM: METHYLOMONAS SP.
US-10-320-924-16

Query Match 100.0%; Score 2284; DB 16; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.4e-223;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVTWPHLTADIRFCHEFLNENFYTLNMPKPKVAILTAGGLAPCLNSAIGSLIRYTE 60
DB 1 DVVTWPHLTADIRFCHEFLNENFYTLNMPKPKVAILTAGGLAPCLNSAIGSLIRYTE 60
QY 61 IDPSIRILCYRGYKGLLDGSDYPTAEVRKAGVLRFGGSVIGNSRVLTNVKDCVCR 120
DB 61 IDPSIRILCYRGYKGLLDGSDYPTAEVRKAGVLRFGGSVIGNSRVLTNVKDCVCR 120
QY 121 GLVGEEDPQKVAADQVLDGVDILHTIGDDTNTAAADLAFLANNYGLTVIGLPTV 180
DB 121 GLVGEEDPQKVAADQVLDGVDILHTIGDDTNTAAADLAFLANNYGLTVIGLPTV 180
QY 181 DNDVPIKOSLGAMTAABOGARYFMNVVAENNANPRLIVHEVMGNCGLTAATQCYR 240
DB 181 DNDVPIKOSLGAMTAABOGARYFMNVVAENNANPRLIVHEVMGNCGLTAATQCYR 240
QY 241 KLDRAEMLPELGLTRESYEVAHVPVEMALIDAEAKRLREVMQKDCVNIIVSSGAGV 300
DB 241 KLDRAEMLPELGLTRESYEVAHVPVEMALIDAEAKRLREVMQKDCVNIIVSSGAGV 300
QY 301 EAIVAEMQAKGQEVPRDAFGHILKDAVNPGRMGEOFAOMIGAEXTLVOKSGYFARASAS 360
DB 301 EAIVAEMQAKGQEVPRDAFGHILKDAVNPGRMGEOFAOMIGAEXTLVOKSGYFARASAS 360
QY 361 NVDNMLIKSCADLAVECAFRESGVIGHEDNNGNTLRAIEPRIRKGRPFNIDTMFNS 420
DB 361 NVDNMLIKSCADLAVECAFRESGVIGHEDNNGNTLRAIEPRIRKGRPFNIDTMFNS 420
QY 421 MLESIQPKGKGVESH 437
DB 421 MLESIQPKGKGVESH 437

RESULT 6
US-10-369-493-14348
Sequence 14348, Application US/10369493
Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14348
LENGTH: 184
TYPE: PRF

ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14348

Query Match 28.9%; Score 659; DB 12; Length 184;
Best Local Similarity 67.9%; Pred. No. 1.1e-58;
Matches 125; Conservative 27; Mismatches 32; Indels 0; Gaps 0;

QY 33 KVALITAGGLAPCLNSAIGSLIERTEIDPSIRICRGYKGLLDDSYVTAVERK 92
DB 1 QVAVMTAGGLAPCLSSAVGSLIERYSIDIAPEIDIAVRSGYQVLLGEIRIETDMERK 60
QY 93 AAVLRFSGSVIGNSRVKLTNVKDCVKGGLVEGEDPOKVAADOLVKQVDLHTIGDD 152
DB 61 AHLIRYGGSPIGNSRVKLTNADCAKGLVEGONPLRVAAERLAADGITLHTIGDD 120
QY 153 TWTAAADLAFLARNNGYGLTVIGLPRYDNDVPPIKOSIGAMTAEGARFPMVAEN 212
DB 121 TWTAAADLAFLAAGANGYDLTVVGLPKTVNDVVPKOSIGAMTAEGAFEDVNSRQS 180
QY 213 AMPR 216
DB 181 AAPK 184

RESULT 7
US-10-369-493-8108

Sequence 8108; Application US/10369493
Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 8108
LENGTH: 350
TYPE: PRP
ORGANISM: Thermobifida fusca
US-10-369-493-8108

Query Match 13.4%; Score 306.5; DB 12; Length 350;
Best Local Similarity 26.5%; Pred. No. 2.2e-22;
Matches 104; Conservative 63; Mismatches 145; Indels 81; Gaps 14;

QY 23 EFPYTLNNKPKKVALITAGGLAPCLNSAIGSLIERTEIDPSIRICRGYKGLLDD 82
DB 4 FKEHYOM---RVGVLTGGGDCPGANAVRAVVRKGIK-EYGYEVGVRDGRGLGDDT 58
QY 83 YVTAVERKAGVLORFSGSVIGNSRVKLTNVKDCVKGGLVEGEDPOKVAADOLVKQV 142
DB 59 WPLDIEAVR--GILPR--GGTILGSSRTMLMKIEGVER-----VQNNMAALGV 103
QY 143 DILHTIGSDTNTAAADLAFLARNNGYGLTVIGLPRYDNDVPPIKOSIGAMTAEGAR 202
DB 104 DALVVAIGSDTLGVANQL-----HDHGVNVGVPEITINDLNAATDYFPGFTAVNATE 157
QY 203 YEMNVVAENNAAPRLIVHVRNGMGLT-----AATAOEYRKLLDRAEMLPELGLTRE 257
DB 158 AIDRLHTTAESHRRALV--EVMGRHAGMTALHAGMAAG-----195
QY 258 STEVAVAVFPEMAIDLEBAKRLRYMKYDCNMFVSGAGVEALVAEMAKQGEVPRD 317
DB 196 ---NVLLIPERFPDDEVAVAYISREKTNVAPITIVAGAPK---EGQULTASAERD 247
QY 318 AFGHIKLDAVNVGKMGEOFAQMIGAETLVOKS---GYFAASASNVDDMLIKSCADL 374

DB 248 SFGEVRLGSI-----QQLAEETIARTGEANSVLGHVORGSTPSAFDRVATRLGLH 301
QY 375 AVECAFRESGVIGHDEDNGNV--LRAIEPRRI 405
DB 302 AITAV-----HDKDFGMVALRGTETIVRV 325

RESULT 8
US-10-156-761-13610

Sequence 13610; Application US/10156761
Publication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13610
LENGTH: 342
TYPE: PRP
ORGANISM: Streptomyces avermitilis
US-10-156-761-13610

Query Match 12.9%; Score 294; DB 15; Length 342;
Best Local Similarity 26.5%; Pred. No. 4e-21;
Matches 101; Conservative 66; Mismatches 140; Indels 74; Gaps 17;

QY 34 KVALITAGGLAPCLNSAIGSLIERTEIDPSIRICRGYKGLLDDSYVTAVERKA 93
DB 2 RVGVLTGGGDCPGANAVIRGVVRKGYQ-EYGYDFVGRDGRGLGDDA--VRDIAVR 58
QY 94 GVLORFGSVIGNSRVKLTNVKDCVKGGLVEGEDPOKVAADOLVKQVDLHTIGDDT 153
DB 59 GILPR--GGTILGSSRTMLPKLDGDIR--IKE-----MLAKQEVALLAIGGDDT 105
QY 154 NTAADLAFLARNNGYGLTVIGLPRYDNDVPPIKOSIGAMTAEGARF--NNVVAEN 211
DB 106 LGVAARLT---DEYGVPAVGVPEITINDLSATDYFPGFTAVGATEALDRHTTAES 160
QY 212 NANPRMLIVHVRNGMGLTAATVQERYRKLDRAEMLPELGLTRSYEVAHAFVPEMAI 271
DB 161 HMR---VLQCEVWGRHAGMTAHS-----GLAGGA---NVLLIPQRF 197
QY 272 DLEAERKLEWMDKVCNMFVSGAGVEALVAEMAKQGEVPR---DAFGIKIDAV 327
DB 198 DVDVCAVYTSRFRASVAPITIVVAGA-----MKDQOMVAKDSLSFGVRLSGV 249
QY 328 NPGKMGEOFAQMIGAS-KTLVQSGYFAPASASNVDDMLIKSCADLAVECAFRESGV 386
DB 250 --GEMLAKEIEKRGKRAITTV--LGHVQGGTSPASDRVLAATFGALHAIEAV-----298
QY 387 IGHDEDNGNV--LRAIEPRRI 405
DB 299 --RDGDFGKVAALGTDIVRV 317

RESULT 9
US-10-156-761-14652

Sequence 14652; Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:

```

APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO: 14652
LENGTH: 341
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-14652

```

```

Query Match 12.5%; Score 284.5; DB 15; Length 341;
Best Local Similarity 27.5%; Pred. No. 3.7e-20;
Matches 97; Conservative 62; Mismatches 143; Indels 51; Gaps 11;

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QY 34 KVALITAGGLAPCLNSAIGSLIERYTEIDPSIEIICRGYKGLLDSDYPTAEVRKA 93
DB 2 RIGVLTSGDCCPGLNNAIVRSVVR-AVVDHDEVIQFEDGKGLLECY-LKLDLAVS 58
QY 94 GVLORFGSGVIGNSRVKLTNVKDCVKGKLVKGEDEPKVAADQVLDGVILHTIGDDT 153
DB 59 GILAR-GGITLSSSRVQPARLRDVER-----ARGHVAEGLDAIIPIGEGT 105
QY 154 NTAADLAFLAFLANNYGLTVIGLPTVNDVFPKISIGAMTAEOGARFYMVAENNA 213
DB 106 LKAARL-----SDAGLPVGVPTKINDIATVDVTFGTAVGATTEALDRKTTAAS 159
QY 214 NPMILVHEVMGRNCGMLTAATQBYRKLDRAMELPELGITRESYEVAHVPEMAIDL 273
DB 160 HQRVLIIV-EVMGRHTGMLALSGM-----AAGAHAVVERPFDI 198
QY 274 EAEKRLREVMDCVNIIF-SSGAGVEAIVAEQAKQGVPRDAPGHILKLDVAFGRM 332
DB 199 EELAKVGERPEAKRRFAIVAAAGAPRACSMDF--DEGKADVGHRRFAGI--ARQ 252
QY 333 FGEQPAQWIGAEKTLVQKSGYFAPASASNVDMKLKSCADLAVECAFRRESG 385
DB 253 LSLLEERLKEARPV-ILGHVQGGTPTATVDRVLATRFGMHAAVEAHRGSEFG 304

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RESULT 10
US-10-156-761-10359
Sequence 10359, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10359

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LENGTH: 341
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-10359

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Query Match 11.8%; Score 269.5; DB 15; Length 341;
Best Local Similarity 26.8%; Pred. No. 1.2e-18;
Matches 96; Conservative 59; Mismatches 142; Indels 61; Gaps 15;

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QY 34 KVALITAGGLAPCLNSAIGSLIERYTEIDPSIEIICRGYKGLLDSDYPTAEVRKA 93
DB 2 RIGVLTSGDCCPGLNNAIVRSVVR-AVVDHDEVIQFEDGKGLLECY-LKLDLAVS 58
QY 94 GVLORFGSGVIGNSRVKLTNVKDCVKGKLVKGEDEPKVAADQVLDGVILHTIGDDT 153
DB 59 GILAR-GGITLSSSRVQPARLRDVER-----ARGHVAEGLDAIIPIGEGT 105
QY 154 NTAADLAFLAFLANNYGLTVIGLPTVNDVFPKISIGAMTAEOGARFYMVAENNA 213
DB 106 LKAARL-----SDAGLPVGVPTKINDIATVDVTFGTAVGATTEALDRKTTAAS 159
QY 214 NPMILVHEVMGRNCGMLTAATQBYRKLDRAMELPELGITRESYEVAHVPEMAIDL 273
DB 160 HQRVLIIV-EVMGRHTGMLALSGM-----AAGAHAVVERPFDI 198
QY 274 EAEKRLREVMDCVNIIF-SSGAGVEAIVAEQAKQGVPRDAPGHILKLDVAFGRM 332
DB 199 EELAKVGERPEAKRRFAIVAAAGAPRACSMDF--DEGKADVGHRRFAGI--ARQ 252
QY 333 FGEQPAQWIGAEKTLVQKSGYFAPASASNVDMKLKSCADLAVECAFRRESG 385
DB 250 GTALAALEHRLKEARPV-ILGHVQGGTPTATVDRVLATRFGMHAAVEAHRGSEFG 304

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RESULT 11
US-10-369-493-19261
Sequence 19261, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19261
LENGTH: 345
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-10-369-493-19261

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Query Match 11.4%; Score 261; DB 12; Length 345;
Best Local Similarity 26.0%; Pred. No. 9.3e-18;
Matches 96; Conservative 66; Mismatches 141; Indels 66; Gaps 16;

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QY 34 KVALITAGGLAPCLNSAIGSLIERYTEIDPSIEIICRGYKGLLDSDYPTAEVRKA 93
DB 2 KVAVLITGGDCCPGLNNAIVRSVVRANA-HGFEMGLRQGMKGLLEDNHRFLTRF--TS 57
QY 94 GVLORFGSGVIGNSRVKLTNVKDCVKGKLVKGEDEPKVAADQVLDGVILHTIGDDT 150
DB 58 GILAR-GGITLSSSRVQPARLRDVER-----ARGHVAEGLDAIIPIGEGT 101
QY 151 DDTNTAADLAFLAFLANNYGLTVIGLPTVNDVFPKISIGAMTAEOGARFYMVAENNA 208
DB 102 EGTLSAATRM-----SOGELRIVGVPTKINDIATVDVTFGTAVGATTEALDRKTTAAS 155

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QY 209 AENNANPRLIVHEWNGCGWLTAAITACEYKLLDRAMELPELGUTRESYEVHAFVPE 268
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 156 AESH---KRVIVCEWVRHVMIAI-----YAGIAGAD-----VILVPE 192
QY 269 MAIDLEAEKRL--REVMDKVCVNIIVSEGGVGEVAIYAEOMAKGOEVRDPAFGHIXIDA 326
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 193 IPADIAKVAEHIQRRRAGGRFISI--VVAEGTRIKLSADQEQSLVTSGLADENGRPLUG 251
QY 327 VNPGEWFGQFQMIKAETLYOKSGYEFARASAVNDKRL-----IKSCADLAVECAFR 381
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 252 V--GTLIAEIERRRGFE--TRSVYGHIRGGAFTAHDRVLTATRYGVAC--DMVARGEG 307
QY 382 RESGVIGHD 390
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 308 KMAALRGND 316

RESULT 12
US-10-369-493-2905
; Sequence 2905, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2905
; LENGTH: 319
; TYPE: PRP
; ORGANISM: Thermotoga maritima
US-10-369-493-2905

Query Match 11.1%; Score 253; DB 12; Length 319;
Best Local Similarity 26.6%; Pred. No. 5,4e-17;
Matches 95; Conservative 60; Mismatches 126; Indels 76; Gaps 14;

QY 33 KVALITAGAGLAPCLNSAIGSLIERTEIDPSIETICRGYKGLLDGSDYPTAEVRKA 92
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 KVALITAGAGLAPCLNSAIGSLIERTEIDPSIETICRGYKGLLDGSDYPTAEVRKA 92
QY 93 AGVLORFGSGVIGNSRVKLTNVKDCVKGRLVKEGSDPQKAAADQLVKDGVDIHTIGGD 152
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 56 AGITRK--GGTILIRRCERFET-----SEGRILAKQIKKGIISGLVIGEG 104
QY 153 TWTAAADLAFLAKNNYGLTVIGLPTVNDVFPPIKOSIGANTAAEGCARFANVAAKN 212
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 105 SUTL-----GAHLIYEHKTPVVGIPATINDIGLIDWCIGVDTCLNTVADAVQKIDTAS 159
QY 211 ANPRLIVHEWNGCGWLTAAITACEYKLLDRAMELPELGUTRESYEVHAFVPEMAID 272
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 160 SHERAFIV--EWGRHSGYIALMAG-----LYTGAE-----AIIVEIIVD 198
QY 273 LEAEAKRELV--MDKVCVNIIVSEGGVGEVAIYAEOMAKGOEVRDPAFGHIXIDA 330
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 199 VSQLDRIIEERRRGRKINSI--IIVAGASATYVAR-----HDE----- 236
QY 331 KMGEGFAQMIKAETLYOKSGYEFARASAVNDKRLIKSCADLAVECAFRSGVIT 387
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 -----YRIGVE--TRITTLHVGQSGSFTAFDRRLALSMGEVAVDALLDGSVDVM 284

RESULT 13
US-10-369-493-9669

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; Sequence 9669, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; LENGTH: 357
; TYPE: PRP
; ORGANISM: Desulfitobacterium hafnense
US-10-369-493-9669

Query Match 11.0%; Score 250.5; DB 12; Length 357;
Best Local Similarity 27.4%; Pred. No. 1.1e-16;
Matches 101; Conservative 63; Mismatches 116; Indels 69; Gaps 17;

QY 34 KVALITAGAGLAPCLNSAIGSLIERTEIDPSIETICRGYKGLLDGSDYPTAEVRKA 93
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 KVALITAGAGLAPCLNSAIGSLIERTEIDPSIETICRGYKGLLDGSDYPTAEVRKA 93
QY 94 GVLORFGSGVIG-----NSRVKLTNVKDCVKGRLVKEGSDPQKAAADQLVKDGVDIHTI 148
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 GLIPLR--GGTILGTNNRNPFAVPTQV-----GERRQVQRSAEVLIRFNAEGIDALIAI 109
QY 149 GSDPTAAADLAFLAKNNYGLTVIGLPTVNDVFPPIKOSIGANT--AAEGCARFAN 206
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 GSDPTAAADLAFLAKNNYGLTVIGLPTVNDVFPPIKOSIGANT--AAEGCARFAN 206
QY 207 VVAENNANPRLIVHEWNGCGWLTAAITACEYKLLDRAMELPELGUTRESYEVHAFV 266
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 164 TTAESH--HRIMLESYGRAGHIAL-----YAGVAGAD-----VILI 200
QY 267 PEMAIDIE--AEAKRLREVMDKVCVNIIVSEGA--GVEAIYAEOMAKGOEVRDPAFGH 321
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 201 PEIYQLESIAEAVORARLKHPSI--IIVAECAKPLGDMV--ERTMSGRTDP----- 252
QY 322 IKLDVAVPKMGFGQF--QMGAEKTYOKSGYEFARASAVNDKRLIKSCADLAVEC 378
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 253 IKLGLT-----GAKLADELKVTDMETRYVTGLHLOQSGSPVAVDVLSTRYGAVAEA 306
QY 379 AFRRESGVI 387
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 ALAGDPGM 315

RESULT 14
US-10-369-493-21998
; Sequence 21998, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374

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SEQ ID NO 21998
 LENGTH: 987
 TYPE: PRT
 ORGANISM: Saccharomyces cerevisiae
 US-10-369-493-21998

Query Match 10.8%; Score 246.5; DB 12; Length 987;
 Best Local Similarity 23.9%; Pred. No. 1.4e-15;
 Matches 103; Conservative 68; Mismatches 135; Indels 125; Gaps 19;

31 KPKKVALITAGGLAPCLNSAIGSLIERYTEIDPSIRIICRYGGYKGLLDSDYPTAVER 90
 204 KKKKIAVMTSGGDSFGMAAVAYVR--TGHEGCVFAYVEGTEGLRGK-----LK 256
 91 KKA-----GLVORGGSVIGSRVYKLTNVKDCVKGGLVKGEDPOKYAADQVYKGV 145
 257 KMAEDVYKGLSR--GGTILGTA-----RSMFEKREGRROAGNLISOGIDAL 303
 146 HTGGDDTNTAAADL-----AFLARNY-----GLTVGLPKTVNDVFP 187
 304 VCGGDSGLT--GADLFHEWPSLVDELVAEGRFKEVAYKSLIVGLSGIDNDMSGT 362
 188 KOSIGAVTAABOGARYMVAENNANPRLIVHEVGRNCGMLT---ATAOERYKXL 243
 363 DSTIGAYSALERICEWVDYIDATKSHSRAVV--EVMGRGCMALMAGIATGADY---- 417
 244 DRAEWLELGTRESYVHAVFVPEMAIDLEAKRLREVMKVDY---NIFVSEKA 298
 418 -----IFPERAVPHGKMODELKEVCQRRSRGRNNNTIIAEBGA 457
 299 -----GVEAIVAKQAEVPRDAFHIKL--DAVNPGRFGFOAQMGAER 345
 458 LDQOLNVTANDYKDALIEL--GLDTKVTILGHVQGGTAVAHDLRLA--LQSVDAVK 512
 346 TLVQKSYFPAASN-----VDNRILKSCADLAVBCAFRBSGVIGHDE 391
 513 AVLS-----FTPEPSPGILGILNKILMPLVESVKLTQSYA-----TAENKOF 557
 392 DNGNVLNIAEF 402
 558 DKXISLRDTEF 568

RESULT 15
 US-09-815-242-13785
 Sequence 13785, Application US/09815242
 Patent No. US20020061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselebeck, Robert
 APPLICANT: Ohlson, Karl L.
 APPLICANT: Zyckind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 1410
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 13785
 LENGTH: 320
 TYPE: PRT
 ORGANISM: Salmonella typhi
 US-09-815-242-13785

Query Match 10.5%; Score 240.5; DB 9; Length 320;
 Best Local Similarity 24.8%; Pred. No. 1e-15;
 Matches 102; Conservative 59; Mismatches 122; Indels 129; Gaps 18;

33 KKVAILITAGGLAPCLNSAIGSLIERYTEIDPSIRIICRYGGYKGL-----LLDGYPTA 87
 3 KKGIVITSGGDAFGMAAIVGVVR--AALTEGLFVGVGYDYLGLYEDRWQIDRYSVD 60
 88 EVKAKAGVLRPGGSGVIGSRVYKLTNVKDCVKGGLVKGEDPOKYAADQVYKGV 147
 61 MNR-----GGTFLGSR--FPEFRD-----ENIRAVAIENLKRIGIDALV 100
 148 IGGDDTNTAAADLAAFLANNYGLTVGLPKTVNDVFPKOSLGAMTAABOGARYFNV 207
 101 IGGDGSYMGAKEL-----TEMGFPICGLPTIIDNDKGTDTIGFTALGVVEAIDRL 154
 208 VANNANPRLIVHEVGRNCGMLTNATQERYKLDRAEKL--BELGLTRESYVHAVF 265
 155 RUTSSHQHISLV--EVMGRYCGDLTLAA-----TAGGEPLTVAVEVEFNR----- 200
 266 VPEMAIDLEAK-----RLREVMKVDVCNIFVSEKAVE--AIVAKQAK 310
 201 -----DLVAELKAGAKKGAIVALTTHMCDVDELAHFIKREGRFTRATYLGHIORG 254
 311 GQSVPRDAFGHKLDAVNPGRFGFOAQMGAERTLVQKSYFPAASASNVDMELIKS 370
 255 GSPVFPYD-----RILASRMAYV----- 272
 371 CADLAVE-----CAFRBSGVIGHDEDNQNVRLATEFPRIRKGRPNIDTQW 417
 273 -IDLILBHGRCVGIQNEQLVHD-----ITDALENK-----RPPK--SDW 312

Search completed: January 29, 2004, 14:43:34
 Job time : 40 secs